

Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 82918, A  
Sequence 7, Appli  
Sequence 2810, Ap  
Sequence 10366, A  
Sequence 15806, A  
Sequence 44, Appl  
Sequence 14554, A  
Sequence 59, Appl  
Sequence 195, App  
Sequence 11512, A  
Sequence 43, Appl  
Sequence 31, Appl  
Sequence 718, App  
Sequence 718, App  
Sequence 3099, Ap  
Sequence 3103, Ap  
Sequence 14763, A  
Sequence 97497, A  
Sequence 97491, A  
Sequence 3094, Ap  
Sequence 3098, Ap  
Sequence 57, Appl  
Sequence 189, Appl  
Sequence 1, Appli  
Sequence 1866, Ap  
Sequence 3101, Ap

15 142.8 2.7 1062 9 US-09-978-729A-1  
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17 142.8 2.7 1062 9 US-09-978-382A-1  
18 142.8 2.7 1062 10 US-09-978-740A-1  
19 137.6 2.6 748 13 US-10-424-599-82918  
20 133.8 2.5 747 10 US-09-849-772-7  
21 130.4 2.4 266 12 US-09-922-293-2810  
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24 123 2.3 5070 9 US-09-853-450-44  
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26 120.8 2.3 906 13 US-10-412-699B-59  
27 120.8 2.3 906 15 US-10-278-536-195  
28 119 2.2 619 17 US-10-021-323-11512  
29 118.8 2.2 5131 9 US-09-853-450-43  
30 117.8 2.2 714 9 US-09-853-450-31  
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33 115.6 2.2 279 12 US-09-922-293-3099  
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39 113.8 2.1 314 12 US-09-922-293-3098  
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41 112.6 2.1 1093 13 US-10-412-699B-57  
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43 112 2.1 3673778 15 US-10-312-841-1  
44 111.4 2.1 244 12 US-09-922-293-1866  
45 111.4 2.1 265 12 US-09-922-293-3101

ALIGNMENTS

RESULT 1

US-09-922-293-21  
; Sequence 21, Application US/099222293  
; Publication No. US20040123339A1  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Transcription in Plants  
; FILE REFERENCE: 16517.254  
; CURRENT APPLICATION NUMBER: US/09/922,293  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/067,000  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: US 60/069,472  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: US 60/071,479  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: US 60/074,201  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,282  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,280  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,281  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,566  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,567  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,565  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/075,462  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/074,789  
; PRIOR FILING DATE: 1998-02-19

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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11039.933 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6681306

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	313.4	5.8	410	12	US-09-922-293-21
2	303.8	5.7	1054	10	US-09-849-772-3
3	303.8	5.7	1057	9	US-09-853-450-1
4	188.2	3.5	794	9	US-09-853-450-3
5	173.8	3.2	768	9	US-09-853-450-5
6	163.4	3.0	779	9	US-09-853-450-9
7	156.2	2.9	756	9	US-09-853-450-13
8	153	2.9	756	9	US-09-853-450-11
9	152.6	2.8	970	13	US-10-425-114-18693
10	151.8	2.8	1210	13	US-10-425-114-20049
11	151.8	2.8	1240	13	US-10-424-599-82915
12	150.2	2.8	697	17	US-10-767-795-5780
13	145.8	2.7	969	13	US-10-424-599-33823
14	142.8	2.7	1062	9	US-09-978-730-1

	Query Match	5.8%	Score 313.4	DB 12	Length 410
	Best Local Similarity	99.7%	Pred. No. 1e-49		
	Matches 314	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	1713	GA AAAA CTTT CCTA ATGGTTCATACAAAGCTGAGCTCTCTTTATATCTCTCTTGTA	1772		
Db	1	GA AAAA CTTT CCTA ATGGTTCATACAAAGCTGAGCTCTCTTTATATCTCTCTTGTA	60		
QY	1773	GT TTTCTTATATGGGGGCTTTGTTTCTTTTGTGTTCTTTTAGAGTAAGAAGTTCTTAAAAA	1832		
Db	61	GT TTTCTTATATGGGGGCTTTGTTTCTTTTGTGTTCTTTTAGAGTAAGAAGTTCTTAAAAA	120		

QY 1833 AGGATCAAAATCGGAGGGGTAGGTTCAATTGAAGAGATAGAGAAACAAGATCAATAG 1892  
Db |||||  
QY 121 AGGATCAAAATCGGAGGGGTAGGTTCAATTGAAGAGATAGAGAAACAAGATCAATAG 180  
Db |||||  
QY 1893 ACAAGTGACATTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGT 1952  
Db |||||  
QY 181 ACAAGTGACATTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGT 240  
Db |||||  
QY 1953 TCTCTGTGATCGAAGTCTCTCTGTGTCTCTCCCATAGGGGAAACTCTTCGAATA 2012  
Db |||||  
QY 241 TCTCTGTGATCGAAGTCTCTCTGTGTCTCTCCCATAGGGGAAACTCTTCGAATA 300  
Db |||||  
QY 2013 CTCACCTGATTCGT 2027  
Db |||||  
QY 301 CTCACCTGATTCGT 315  
Db |||||

RESULT 2  
US-09-849-772-3  
; Sequence 3, Application US/09849772  
; Publication No. US20030167539A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin  
; APPLICANT: Weigel, Detlef  
; TITLE OF INVENTION: GENETICALLY MODIFIED PLANTS HAVING  
; TITLE OF INVENTION: MODULATED FLOWER DEVELOPMENT  
; FILE REFERENCE: SALKINS.7CPIC2  
; CURRENT APPLICATION NUMBER: US/09/849,772  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: 09/204,094  
; PRIOR FILING DATE: 1998-12-01  
; PRIOR APPLICATION NUMBER: 08/827,332  
; PRIOR FILING DATE: 1997-03-25  
; PRIOR APPLICATION NUMBER: 08/576,156  
; PRIOR FILING DATE: 1995-12-21  
; PRIOR APPLICATION NUMBER: 08/360,336  
; PRIOR FILING DATE: 1994-12-21  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1054  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (124)...(891)  
US-09-849-772-3

Query Match 5.7%; Score 303.8; DB 10; Length 1054;  
Best Local Similarity 99.3%; Pred. No. 1.2e-47;  
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1721 TTCCTAATGGTTCATACCAAGTCTGAGCTCTTTTATATCTCTCTGTAGTTCTTA 1780  
Db |||||  
QY 1781 TTGGGGGTCTTTGTTTGTCTTTTGAAGTAAGAGTTCTTAAAAAGGATCAA 1840  
Db |||||  
QY 1841 AAATGGGAGGGGTAGGTTCAATTGAAGATAGAGAAACAAGATCAATAGACAAGTGA 1900  
Db |||||  
QY 122 AAATGGGAGGGGTAGGTTCAATTGAAGATAGAGAAACAAGATCAATAGACAAGTGA 181  
Db |||||  
QY 1901 CATTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTGTG 1960  
Db |||||  
QY 182 CATTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTGTG 241  
Db |||||  
QY 1961 ATGCTGAAGTCTCTGTGTCTCTCCCATAGGGGAAACTCTTCGAATACTCCACTG 2020  
Db |||||  
QY 242 ATGCTGAAGTCTCTGTGTCTCTCCCATAGGGGAAACTCTTCGAATACTCCACTG 301  
Db |||||

QY 2021 ATCTTGT 2027  
Db |||||  
QY 302 ATCTTGT 308  
Db |||||  
RESULT 3  
US-09-853-450-1  
; Sequence 1, Application US/09853450  
; Publication No. US20020194645A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Pelaz, Soraya  
; APPLICANT: Ditta, Gary  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants  
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development  
; FILE REFERENCE: 19452A-002400US  
; CURRENT APPLICATION NUMBER: US/09/853,450  
; CURRENT FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: Patencin ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1057  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (124)...(894)  
; OTHER INFORMATION: APETALAI (AP1)  
US-09-853-450-1

Query Match 5.7%; Score 303.8; DB 9; Length 1057;  
Best Local Similarity 99.3%; Pred. No. 1.2e-47;  
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1721 TTCCTAATGGTTCATACCAAGTCTGAGCTCTTTTATATCTCTCTGTAGTTCTTA 1780  
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QY 1781 TTGGGGGTCTTTGTTTGTCTTTTGAAGTAAGAGTTCTTAAAAAGGATCAA 1840  
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QY 1841 AAATGGGAGGGGTAGGTTCAATTGAAGATAGAGAAACAAGATCAATAGACAAGTGA 1900  
Db |||||  
QY 122 AAATGGGAGGGGTAGGTTCAATTGAAGATAGAGAAACAAGATCAATAGACAAGTGA 181  
Db |||||  
QY 1901 CATTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTGTG 1960  
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QY 182 CATTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTGTG 241  
Db |||||  
QY 1961 ATGCTGAAGTCTCTGTGTCTCTCCCATAGGGGAAACTCTTCGAATACTCCACTG 2020  
Db |||||  
QY 242 ATGCTGAAGTCTCTGTGTCTCTCCCATAGGGGAAACTCTTCGAATACTCCACTG 301  
Db |||||  
QY 2021 ATCTTGT 2027  
Db |||||  
QY 302 ATCTTGT 308  
Db |||||

RESULT 4  
US-09-853-450-3  
; Sequence 3, Application US/09853450  
; Publication No. US20020194645A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Pelaz, Soraya  
; APPLICANT: Ditta, Gary  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants  
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development  
; FILE REFERENCE: 19452A-002400US  
; CURRENT APPLICATION NUMBER: US/09/853,450

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; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Brassica oleracea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(794)
; OTHER INFORMATION: APETALA1 (AP1)
US-09-853-450-3

Query Match
Best Local Similarity 3.5%; Score 188.2; DB 9; Length 794;
Matches 207; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 1807 TTTTAGAGTAAAGTTCTTAAAGATCAAAATGGAAGGGGTAGGTTCAATTG 1866
Db 1 TCTTAGAGGAATAGTTCCTTTAAAGGGAT-AAAAATGGGAAGGGGTAGGTTCAAGTTG 59

QY 1867 AAGAGGATAGAGAACAGATCAATAGACAGTGCATCTCTCGAAGAGAGCTGGTCTT 1926
Db 60 AAGAGATAGAAACAGATCAATAGACAGTGCATCTCTCGAAGAGAGAGCTGGTCTT 119

QY 1927 TTGAAGAAAGCTCATGAGATCTCTGTTCTGTGATGCTGAAGTTGCTTGTGCTTC 1986
Db 120 ATGAAGAAAGCTCATGAGATCTCTGTTCTGTGATGCTGAAGTTGCTTGTGCTTC 179

QY 1987 TCCATAAGGGGAACTCTCGAATACCTCACTGATCTTG 2027
Db 180 TCCATAAGGGGAACTCTTGAATACCTCACTGATCTTG 220

RESULT 5
US-09-853-450-5
; Sequence 5, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Brassica oleracea var. botrytis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
; OTHER INFORMATION: APETALA1 (AP1)
US-09-853-450-5

Query Match
Best Local Similarity 3.2%; Score 173.8; DB 9; Length 768;
Matches 178; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1843 ATGGGAAGGGGTAGGGTTCAATTGAAGAGGTAGAGAACAGATCAATAGACAGTGACA 1902
Db 1 ATGGGAAGGGGTAGGGTTCAAGTTGAAGAGGTAGAGAACAGATCAATAGACAGTGACA 60

QY 1903 TTCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTGTGAT 1962
Db 61 TTCTCGAAAAGAGAGCTGGTCTTTATGAAGAAAGCTCATGAGATCTCTGTTCTGTGAT 120

QY 1963 CTGAGTGTCTTGTGTCTTCTCCCAATAGGGGAACTCTTCGAATACTCCACTGAT 2022
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Db 121 GCTGAAGTTGGCTTGTGTCTTCTCCATAAGGGGAACTCTTTGAATACCCCACTGAT 180
QY 2023 TCTTG 2027
Db 181 TCTTG 185

RESULT 6
US-09-853-450-9
; Sequence 9, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 779
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(777)
; OTHER INFORMATION: CAULIFLOWER (CAL)
; NAME/KEY: modified_base
; LOCATION: (778)..(779)
; OTHER INFORMATION: n = g, a, c or t
US-09-853-450-9

Query Match
Best Local Similarity 3.0%; Score 163.4; DB 9; Length 779;
Matches 173; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1839 AAAAAATGGGAAGGGGTAGGGTTCAATTGAAGAGGTAGAGAACAGATCAATAGACAGT 1898
Db 6 AGAAATGGGAAGGGGTAGGGTTCAATTGAAGAGGTAGAGAACAGATCAATAGACAGT 65

QY 1899 GACATTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTTG 1958
Db 66 GACATTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTTG 125

QY 1959 TGATGCTGAAGTTGCTTGTGTTCTTCTCCATAAGGGGAACTCTTCGAATACTCCAC 2018
Db 126 TGATGCGAGGGTTCCCTTATTTGTTCTTCCATAAGGGGAACTTTGTCGAGTACTCTC 185

QY 2019 TGATTTCTTG 2027
Db 186 TGAATCTTG 194

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; Sequence 13, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
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; SEQ ID NO 20049  
; LENGTH: 1210  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB170-041-G10\_F11  
US-10-425-114-20049

Query Match 2.8%; Score 151.8; DB 13; Length 1210;

Best Local Similarity 71.0%; Pred. No. 1.2e-18; Indels 0; Gaps 0;  
Matches 201; Conservative 0; Mismatches 82;

QY 1745 CTGAGCTCTCTTTATATCTCTCTGTAGTTCTTATTTGGGGTCTTTGTTTGGTTGGT 1804

Db 187 CTCACCTCTTAGGGTTATTTTGTCTCCCTTTTCTTGTGGGAATTGGGTTGGTTGGT 246

QY 1805 TCTTTTAGAGTAAGAGTTCTTAAAAAGGATCAAAATGGAAGGGGTAGGGTTCAAT 1864

Db 247 TTTTCTGTGTGTAAGAAAGAAACAAAGAAAGAACTAAGATGGAAGAGGTAGGGTACAGC 306

QY 1865 TGAAGAGGATAGAGAAACAAGATCAATAGACAAGTGCATTTCTGAAAAGAGCTGGTC 1924

Db 307 TGAAGAGGATAGAGAAACAAGATCAATGCGAGTAATTTCTCCAAAGAGAGGTGGGT 366

QY 1925 TTTTGAAGAAAGCTCATGATCTCTTCTCTGTGATGCTGAAGTTGCTTCTTGTGCT 1984

Db 367 TGTCTAAGAAAGCTCATGAAATCTGTACTCTGTGATGCTGAGGTAGCTTTGATTATCT 426

QY 1985 TCTCCNTAAGGGAAACTCTCGAATCTCCTCACTCACTGATTCTTG 2027

Db 427 TCTCTCAAGAAAGAGCTCTTTGAGTATGCTACTGATTCAATG 469

## RESULT 11

US-10-424-599-82915

; Sequence 82915, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 82915

; LENGTH: 1240

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_45890C.1

US-10-424-599-82915

Query Match

Best Local Similarity 2.8%; Score 151.8; DB 13; Length 1240;

Matches 201; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 1745 CTGAGCTCTCTTTATATCTCTCTGTAGTTCTTATTTGGGGTCTTTGTTTGGTTGGT 1804

Db 199 CTCACCTCTTAGGGTTATTTTGTCTCCCTTTTCTTGTGGGAATTGGGTTGGTTGGT 258

QY 1805 TCTTTTAGAGTAAGAGTTCTTAAAAAGGATCAAAATGGAAGGGGTAGGGTTCAAT 1864

Db 259 TTTTCTTGTGTAAGAAAGAAACAAGAAAGAACTAAGATGGAAGAGGTAGGGTACAGC 318

QY 1865 TGAAGAGGATAGAGAAACAAGATCAATAGACAAGTGCATTTCTGAAAAGAGAGCTGGTC 1924

Db 319 TGAAGAGGATAGAGAAACAAGATCAATGCCAGGTAATTTCTCCAAAGAGAGGTGGGT 378

QY 1925 TTTTGAAGAAAGCTCATGAGATCTCTGTCTCTGTGATGCTGAAGTGTCTTGTGCT 1984

Db 379 TGCTCAGAAAGCTCATGAATATCTGTACTCTGTGATGCTGAGTAGCTTTGATTATCT 438

QY 1985 TCTCCCATTAAGGGAAACTCTTCGAATATCTCCACTGATTTCTTG 2027

Db 439 TCTCTCACAAGAGAAAGCTCTTTGAGTATGCTACTGATTCATG 481

## RESULT 12

US-10-767-795-5780

; Sequence 5780, Application US/10767795

; Publication No. US20040181830A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Cao, Yongwei

; APPLICANT: Zhou, Yihua

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53534)B

; CURRENT APPLICATION NUMBER: US/10/767,795

; CURRENT FILING DATE: 2004-01-30

; NUMBER OF SEQ ID NOS: 117596

; SEQ ID NO 5780

; LENGTH: 697

; TYPE: DNA

; ORGANISM: Gossypium hirsutum

; FEATURE:

; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C8942\_1

US-10-767-795-5780

Query Match

Best Local Similarity 2.8%; Score 150.2; DB 17; Length 697;

Matches 192; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1827 TAAAAAAGGATCAAAAATGGGAGGGGTAGGGTTCAATTGAAGAGGATAGAACCAAGAT 1886

Db 121 TATTTAAAAAAAATCATGGGAAGAGGTAGGGTTCAATTTAAAAAGGATTGAAAAACAAGAT 180

QY 1887 CAATAGACAAGTCACATCTCCAAAAGAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGAT 1946

Db 181 CAACAGACAAGTTACTTTTCCAAAAGAGAGCTGGTTTATTTGAAAAAAGCTCATGAGAT 240

QY 1947 CTCTGTCTCTGTGATGCTGGAAGTTGCTCTTCTGTCTCTCCATAAGGGGAACTCTT 2006

Db 241 CTCTGTCTTCTGTGATGCTGGAAGTTGCTCTTCTGTCTCTCCATAAGGGGAACTCTT 300

QY 2007 CGAATACCTCACTGATTTCTTGTAATCTCACTCACTCACTTTTAAAAAAAT 2061

Db 301 TGAGTACTCCACTGATTTCTGTATGGAAGAGATCTTGAAACGCTATGAAAGGTAT 355

## RESULT 13

US-10-424-599-33823

; Sequence 33823, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 33823

; LENGTH: 969

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_130546C.1

US-10-424-599-33823

	Query Match	2.7%;	Score 145.8;	DB 13;	Length 969;
	Best Local Similarity	75.9%;	Pred. No. 1.5e-17;		
	Matches 180;	Conservative 0;	Mismatches 57;	Indels 0;	Gaps 0;
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DB	221	AGGATGAGAACAGATCAATCGCGAGGTAACTTTCT	CCAAAAGGACAGCTGGTCTACTC	280	
QY	1930	AAGAAAGCTCATCAGATCTCTGTCTCTGTGATGCTGAAGTTC	GTCTGTGTGTGCTCTCTCC	1989	
DB	281	AAGAAAGCACAGAGATCTCTGTCTCTGTGACGTGAGTTCG	TTTGATTTGCTCTCTCC	340	
QY	1990	CATAAGGGGAACTCTTCGAATACTCACTGATTC	TGTGGTAACCTCAATTC	2046	
DB	341	CACAAAGGAAGCTCTTTGAATATGCCCGATCTTGGTAA	TTAAATATATATCAT	397	

## RESULT 14

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US-09-978-730-1
; Sequence 1, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000920US
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-730-1

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US-09-978-729A-1
; Sequence 1, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-729A-1

Query Match      2.7%; Score 142.8; DB 9; Length 1062;
Best Local Similarity 81.7%; Pred. No. 6e-17;
Matches 165; Conservative 0; Mismatches 37; Indels 0; Gaps 0

Qy      1826  TTTAAAAAGCATCAAAAATGGGAAGCGGTAGGGTTTCAATTGAAGAGGATAGAGAACAGA 188
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Qy      1886  TCAATAGA CAAGTGACATTTCTCGAAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGA 194
Db      144   TCAATAGGCAAGTTACTTTTCTCAAAAGAGAAAGGCTCTGGTTGCTCAAGAAAGCTCATGAGA 208
Qy      1946  TCTCTGTTCTCTGTGATGCTGAAGTTGCTCTGTGTTGCTCTTCTCCCATAAAGGGAACTCT 200
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Qy      2006  TCGAATACTCCCACTGATTTTG 2027
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RESULT 15

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 18:50:20 ; Search time 12353 Seconds  
(without alignments)  
12976.620 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- EST:\*
- 1: em\_estba:\*
  - 2: em\_esthum:\*
  - 3: em\_estin:\*
  - 4: em\_estm:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_htc:\*
  - 9: gb\_est1:\*
  - 10: gb\_est2:\*
  - 11: gb\_htc:\*
  - 12: gb\_est3:\*
  - 13: gb\_est4:\*
  - 14: gb\_est5:\*
  - 15: em\_estfun:\*
  - 16: em\_estom:\*
  - 17: em\_gss\_hum:\*
  - 18: em\_gss\_inv:\*
  - 19: em\_gss\_pln:\*
  - 20: em\_gss\_vrt:\*
  - 21: em\_gss\_fun:\*
  - 22: em\_gss\_mam:\*
  - 23: em\_gss\_mus:\*
  - 24: em\_gss\_pro:\*
  - 25: em\_gss\_rod:\*
  - 26: em\_gss\_phg:\*
  - 27: em\_gss\_vrl:\*
  - 28: gb\_gss1:\*
  - 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	405.8	7.6	426	28	BH240291	BH240291 AUNAG62TR
3	356.4	6.6	383	28	BH240405	BH240405 AUNAG34TR
4	325.4	6.1	638	9	AU236519	AU236519 AU236519

5	316	5.9	509	9	AA067443	AA067443 26288 Lam
6	189.6	3.5	676	28	BH994331	BH994331 oeg92a11
7	176.2	3.3	646	28	BZ503616	BZ503616 BONAV25TR
8	162.4	3.0	779	28	BZ065259	BZ065259 11f48b05
9	160.2	3.0	503	9	AI992862	AI992862 701493815
10	150.2	2.8	694	28	BZ004972	BZ004972 oel176b05
11	148.8	2.8	813	29	CC946428	CC946428 BOIFJ10TF
12	148	2.8	811	28	BZ484352	BZ484352 BON0214TR
13	147	2.7	476	14	T42418	T42418 5681 Lambda
14	145.2	2.7	658	12	BG456966	BG456966 NF08D09P
15	145.2	2.7	665	12	BI263356	BI263356 NF089C12P
16	145.2	2.7	830	28	BH249426	BH249426 BOGAK13TR
17	143.8	2.7	440	9	AI100509	AI100509 34884 Lam
18	142.8	2.7	543	14	CB258385	CB258385 30-E01180
19	142.8	2.7	559	14	CB258393	CB258393 30-E01179
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21	139.6	2.6	200	29	BX288612	BX288612 Arabidops
22	138.6	2.6	353	14	CF510214	CF510214 USDA-FP 1
23	138.6	2.6	414	14	CF508545	CF508545 USDA-FP 1
24	138.6	2.6	626	14	CF507975	CF507975 USDA-FP 1
25	137	2.6	850	10	AW738740	AW738740 EST340167
26	136.6	2.5	734	13	B0872670	B0872670 Q045E11 P
27	135.6	2.5	680	13	BQ148488	BQ148488 NF068H07F
28	135.4	2.5	615	13	B0868189	B0868189 M112C09 P
29	134.4	2.5	550	13	B0995541	B0995541 QG10E16
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33	130.8	2.4	467	10	AW266670	AW266670 LO-1492T3
34	130.8	2.4	707	10	BF479063	BF479063 L48-2708T
35	130	2.4	634	14	CA917484	CA917484 EST641631
36	129.8	2.4	777	10	BE034098	BE034098 MG05B05 M
37	129.2	2.4	694	10	BF479099	BF479099 L48-2745T
38	128.4	2.4	755	13	BQ988395	BQ988395 QGF14M24
39	128.2	2.4	613	12	BM406322	BM406322 EST580649
40	127.2	2.4	331	14	CA525666	CA525666 KS1205980
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42	125.2	2.3	505	14	CF508148	CF508148 USDA-FP 1
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ALIGNMENTS

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DEFINITION survey sequence.  
ACCESSION B97569  
VERSION B97569.1 GI:2999648  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids;  
1 (bases 1 to 435)  
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K.,  
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and  
Venter,J.C.  
A BAC End Sequence Database for Identifying Minimal Overlaps in  
Arabidopsis Genomic Sequencing. Update 3  
Unpublished (1997)  
Contact: Steve Rounsley  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: rounsley@tigr.org

Seq primer: M13-21

Class: BAC ends

High quality sequence stop: 435.

Location/Qualifiers

## FEATURES

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/mol\_type="genomic DNA"

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/db\_xref="taxon:3702"

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/note="Vector: BelOBACII; Site\_1: EcoRI; Site\_2: EcoRI;

Produced by Thomas Altmann"

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QY 2458 TAGTAAGAAATAAAGATCTGTAGTTTTCACCTCGCTCACTGAGTTCGAGTTTAAATGAAG 2517  
 Db 61 TAGTAAGAAATAAAGATCTGTAGTTTTCACCTCGCTCACTGAGTTCGAGTTTAAATGAAG 120

QY 2518 TGTCTGTTCTTTTTCATATAT-AGTTGCAACTGGAATTAATTAATAATTAATTAATGAAG 2576  
 Db 121 TGTCTGTTCTTTTTCATATATAGTTGCAACTGGAATTAATTAATAATTAATTAATGAAG 180

QY 2577 CGAGAAATAATTTAAATAGATATAGATAACAATGTCAAATGTCAAATGTCAAATGTCAAATGTC 2636  
 Db 181 CGAGAAATAATTTAAATAGATATAGATAACAATGTCAAATGTCAAATGTCAAATGTC 240

QY 2637 AAGATATTTAACTTACGAGTTGTTTTCAGCTGTGTAAGAAATATCTAATTTGTTCT 2696  
 Db 241 AAGATATTTAACTTACGAGTTGTTTTCAGCTGTGTAAGAAATATCTAATTTGTTCT 300

QY 2697 CACGACTGTCTTCATGTTTTCGAAATCTAAGCAAGAAATGTTTAACTCGGATCTT 2756  
 Db 301 CACGACTGTCTTCATGTTTTCGAAATCTAAGCAAGAAATGTTTAACTCGGATCTT 360

QY 2757 AAGATTATGAACCTGTAATATAAAACACTATATAGTATTAAATTTGAACTAGTGTGCTT 2816  
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QY 2817 CTTTGTGCTACTT 2828  
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 DEFINITION BH240291 AUIN Arabidopsis thaliana genomic clone AUIN62, genomic survey sequence.  
 ACCESSION BH240291.1 GI:16913649  
 VERSION BH240291  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 426)  
 Town, C.D., Whitelaw, C.A., Pai, G., Van Aken, S.E., Utterback, T.V., Feldblyum, T.V. and Fraser, C.M.  
 Survey sequencing of Arabidopsis thaliana BAC T17015  
 Unpublished (2001)  
 Other GSSs: AUIN62TF  
 Contact: Chris Town

## TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

From Wash. U contig 1128.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..426

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia"

/db\_xref="taxon:3702"

/clone="AUIN62"

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/note="Vector: pHOS2; Site\_1: BstXI; 2-3 kb sheared BAC

DNA inserted into pHOS2 using BstXI linkers"

## ORIGIN

Query Match 7.6%; Score 405.8; DB 28; Length 426;  
 Best Local Similarity 99.3%; Pred. No. 2.9e-42;  
 Matches 418; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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 Db 6 AATCTGAGTAGGAGCTCTTTGACCTCTGGGATCCATAAAAAAGAACTAATCCATCTAA 65

QY 2924 AATCGGCTTCTTACCGATGGTCAAACTTAGCTCCCAAGCAAGCAAGCTGTTCTCTTTT 2983  
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QY 3163 ATTCACTACTGTTTGTATTATTAAGGATCATAGAGATCGGTACTTGTATTGTATAGG 3222  
 Db 306 ATTCACTACTGTTTGTATTATTAAGGATCATAGAGATCGGTACTTGTATTGTATAGG 365

QY 3223 AAATCTTGGTTTAAATTTGCATAAAACCATTAGATTATCTTAAATGTGATGATATTT 3282  
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QY 3283 T 3283  
 Db 426 T 426

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 VERSION BH240405.1 GI:16913879  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 383)  
 Town, C.D., Whitelaw, C.A., Pai, G., Van Aken, S.E., Utterback, T.V., Feldblyum, T.V. and Fraser, C.M.

TITLE Survey sequencing of Arabidopsis thaliana BAC T17J15  
JOURNAL Unpublished (2001)  
COMMENT Other\_GSSs: AUNA34TF  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
From Wash. U contig I128.  
Seq primer: TR  
Class: sheared ends.

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		DNA inserted into PHOS2 using Bst

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ACCESSION	
VERSION	AU236519.1 GI:19875688
KEYWORDS	EST.
SOURCE	Arabidopsis thaliana (chale cross)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses. 1 (bases 1 to 638)
AUTHORS	Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,

Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@tc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda  $\lambda$  vector (Garrinci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified Bluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

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Qy	1821	GTTCCTTTAAAAAGGATCAAAAATGGGAAGGGGTAGGGTTCAAATTGAAGAGGATAGAA	1880		
Db	121	GTTCCTTTAAAAAGGATCAAAAATGGGAAGGGGTAGGGTTCAAATTGAAGAGGATAGAA	180		
Qy	1881	CAAGATCAATAGACAAGTGACATTCCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCA	1940		
Db	181	CAAGATCAATAGACAAGTGACATTCCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCA	240		
Qy	1941	TGAGATCTCTGTTCTCTGTGATGCTGAAGTTGCTCTTGTGTCTTCTCCCAATAAGGGAA	2000		
Db	241	TGAGATCTCTGTTCTCTGTGATGCTGAAGTTGCTCTTGTGTCTTCTCCCAATAAGGGAA	300		
Qy	2001	ACTCTTCGAATACTCCACTGATCTTG 2027			
Db	301	ACTCTTCGAATACTCCACTGATCTTG 327			

RESULT 5	AA067443	509 bp	linear	EST 06-NOV-1999		
LOCUS	AA067443	26288	Arabidopsis thaliana cDNA clone 91D3T7, mRNA			
DEFINITION	sequence.					
ACCESSION	AA067443					
VERSION	AA067443.1	GI:1565776				
KEYWORDS	EST.					
SOURCE	Arabidopsis thaliana (thale cress)					
ORGANISM	Arabidopsis thaliana					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.					
	1 (bases 1 to 509)					

**AUTHORS** Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas, M., Retzel, B., and Somerville, C.  
**TITLE** Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
**JOURNAL** Plant Physiol. 106, 1241-1255 (1994)  
**MEDLINE** 95148729  
**PUBMED** 7846151  
**COMMENT** Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313tcn@bm.cl.msu.edu  
 Seq primer: T7 dye primer.  
 Location/Qualifiers  
 1..509

# FEATURES

source  
 1..509  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /strain="var columbia"  
 /db\_xref="taxon:3702"  
 /clone="g1D3T7"  
 /clone\_lib="Lambda-PRL2"  
 /note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dr primed cDNA."

# ORIGIN

Query Match 5.9%; Score 316; DB 9; Length 509;  
 Best Local Similarity 99.7%; Pred. No. 6.2e-31;  
 Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1711 AAAAACTTCTCTTAATGGTCTATACCAAGCTCGAGCTCTCTTTATATCTCTTG 1770  
 Db 1 AAAAAAACTTCTCTTAATGGTCTATACCAAGCTCGAGCTCTCTTTATATCTCTTG 60  
 QY 1771 TAGTTCTTATGGGGCTTTGTTTGTGTTGTTTGTAGTAAGAAGTTCTTAAA 1830  
 Db 61 TAGTTCTTATGGGGCTTTGTTTGTGTTGTTTGTAGTAAGAAGTTCTTAAA 120  
 QY 1831 AAAGGATCAAAAATGGGAAGGGTGAAGGTTCAATTGAAGAGATAGAGAACAGATCAAT 1890  
 Db 121 AAAGGATCAAAAATGGGAAGGGTGAAGGTTCAATTGAAGAGATAGAGAACAGATCAAT 180  
 QY 1891 AGACAAGTGACATTTCTGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCT 1950  
 Db 181 AGACAAGTGACATTTCTGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCT 240  
 QY 1951 GTTCTCTGTGATGCTGAAGTTGCTTCTGTTCTTCTCCCATAGGGGAACTCTTCGAA 2010  
 Db 241 GTNCTCTGTGAAGTGAAGTTGCTTCTGTTCTTCTCCCATAGGGGAACTCTTCGAA 300  
 QY 2011 TACTCCACTGATTTCTTG 2027  
 Db 301 TACTCCACTGATTTCTTG 317

RESULT 6  
 BH994331/c  
 LOCUS oeg92a11.b1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.  
 DEFINITION BH994331  
 ACCESSION BH994331  
 VERSION BH994331.1 GI:23536443

# KEYWORDS

SOURCE ORGANISM  
 Brassica oleracea

# REFERENCE

AUTHORS Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.  
 TITLE Whole genome shotgun reads from Brassica oleracea  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Richard K. Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@watson.wustl.edu  
 Plate: oeg92 row: a column: 11  
 Seq primer: -21UpPOT forward  
 Class: shotgun  
 High quality sequence stop: 537.

# FEATURES

source  
 1..676  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3712"  
 /clone\_lib="B.oleracea002"  
 /note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T0100DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

# ORIGIN

Query Match 3.5%; Score 189.6; DB 28; Length 676;  
 Best Local Similarity 78.1%; Pred. No. 5.5e-15;  
 Matches 253; Conservative 0; Mismatches 69; Indels 2; Gaps 2;  
 QY 3300 TATTTATATATAAATGATAATGGTTGATGATATAAGCTAACCTTAATTTCTGTGAAATG 3359  
 Db 359 TATATATATATGATAATAAATGATGATGATATAAGCTAACCTTAATTTCTGTGAAATG 300  
 QY 3360 ATCAGTAGGAGAGAGATACCTTGAACGCTATGAGGTTACTCTTACGCCGAAGACAGCTT 3419  
 Db 299 AACAGTAGGAGAGAGATACCTTGAACGCTATGAGGTTACTCTTACGCCGAAGACAGCTT 240  
 QY 3420 ATTGCACCTGAGTCCGAGCTCAATGCTATTTCAATAAATATTTCTCTTTTAAAT-CCACAT 3478  
 Db 239 ATTGCACCTGAGTCCGAGCTCAATGCTAATTAATCAATATCTCTCCATTAGCTAAGTGACATAC 180  
 QY 3479 ATATATTATATCAATCTATTTGTTAGTATTTGATGAATTTTATTTGTA-TAAACCTTCTGGT 3537  
 Db 179 ACTATATATAAATATCTCTTTCCAGTATATCTGAAATATATCTGTATTAAACCTTTTGAG 120  
 QY 3538 ACACAGACAAACTCGTCTGATGGAGTATAACAGGCTTAAGGCTTAAGCTTAAGCTTTTGAG 3597  
 Db 119 ACACAGACAAACTCGTCAATGGAGTACAACAGGCTTAAGGCTTAAGCTTTTGAG 60  
 QY 3598 AGAAACCAGAGGTACACATTTTACA 3621  
 Db 59 AGAAACCAGAGGTACATCTTGCA 36

# RESULT 7

BZ503616  
 LOCUS BONAV25TR BO 1.6 2 KB tot Brassica oleracea genomic clone BONAV25,  
 DEFINITION genomic survey sequence.  
 ACCESSION BZ503616  
 VERSION BZ503616.1 GI:27022224  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 646)  
Town, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of *Brassica oleracea*

Unpublished (2001)

Other GSSs: BONAV25TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

FEATURES

Location/Qualifiers

1..646

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/strain="TO1000DH3"

/db\_xref="taxon:3712"

/clone="BONAV25"

/clone\_lib="BO\_1.6\_2\_KB\_tot"

/notes="Vector: pHO51; Site 1: BstXI; 1.6-2 kb sheared

total DNA inserted into pHO51 using BstXI linkers"

## ORIGIN

Query Match 3.3%; Score 176.2; DB 28; Length 646;  
Best Local Similarity 72.3%; Pred. No. 2.8e-13;  
Matches 284; Conservative 0; Mismatches 103; Indels 6; Gaps 4;  
QY 4681 TGSCAGATCAAGGAGGAGGAAAAATCTTAGGGCTCAACAGCAGCAGATGGGATCAGCAG 4740  
DB 258 TGTGAGATTAGGAGAGGAGGAAAAAGCTTCTTAGGGCGCAACAGAGCAATGGGACGAGCAG 317  
QY 4741 AACCAAGGCCACAAATATGCTCCCTCTGCCACCGCAGCAGCACCACAAATCCAGCATCTCT 4800  
DB 318 AACCATGGCCATAATATGCTCCGCTCCACCCCGCAGCAGCATCAATCCAGCATCTCT 377  
QY 4801 TACATGCTCTCATCAGCCATCTCTCTTCTCAACATGGGGTAAACAAAAATCTACTAAT 4860  
DB 378 TACATGCTCTCATCAGCCATCTCTCTTCTCAACATGGGGTAAAT---TCGT 434  
QY 4861 CAGCTCTTAATTTAAAGCACATATGTTATGCA-AGCTAGTTACGTTAGGTGTTGTAATTC 4919  
DB 435 TCCTCTTACTTTCAAGTACATATGTTATATATACAGATAGTTAGGTGTTATAGTCC 494  
QY 4920 ATTGAAGTTATAGCTGTAGTGTAGTTATCATGATGCTAGATTTTGAACCTAGAAACTT 4979  
DB 495 AGTGAGTTAGGTGTTGTTAGTGTAGTTAGTGTCTAAATTTGTAATTACAAGTACTAAG 554  
QY 4980 TATTTTAAACAT-TATTTTAACTAGGTAAATCAATGTTGTCGCCAACGACAAAC 5038  
DB 555 ATTTTTCATGTATATATAAGTATTCATCAATCAATCAATGTTGCGTAAATAAACAGAC 614  
QY 5039 TTATTAGTGGGAAAAATGTACATGGAATGTT 5071  
DB 615 TTATTATTTTGGGAAA-ATAGATGGAATGGCT 646

RESULT 8  
BZ065259  
LOCUS BZ065259 779 bp DNA linear GSS 10-OCT-2002  
DEFINITION BZ065259.1 B.oleracea002 Brassica oleracea genomic, genomic survey  
sequence.  
ACCESSION BZ065259  
VERSION BZ065259.1 GI:23677747  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 779)

Delehaunty, K., Fewell, G., Fulton, D., McCombie, W.R., Miner, T.,

Nash, W., Rabinowicz, P.D. and Wilson, R.K.

Whole genome shotgun reads from *Brassica oleracea*

Unpublished (2002)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: 11f48 row: b column: 05

Seq primer: -21UPOT forward

Class: shotgun

High quality sequence start: 17

High quality sequence stop: 551.

Location/Qualifiers

1..779

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/db\_xref="taxon:3712"

/clone\_lib="B.oleracea002"

/note="Vector: pOTW13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using *Brassica oleracea* TO1000DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

## ORIGIN

Query Match 3.0%; Score 162.4; DB 28; Length 779;  
Best Local Similarity 68.9%; Pred. No. 1.4e-11;  
Matches 259; Conservative 0; Mismatches 101; Indels 16; Gaps 2;  
QY 4681 TGSCAGATCAAGGAGGAGGAAAAATCTTAGGGCTCAACAGCAGCAGATGGGATCAGCAG 4740  
DB 183 TGTGAGATTAGGAGAGGAGGAAAAAGCTTCTTAGGGCGCAACAGAGCAATGGGACGAGCAG 242  
QY 4741 AACCAAGGCCACAAATATGCTCCCTCTGCCACCGCAGCAGCACCACAAATCCAGCATCTCT 4800  
DB 243 AACCATGGCCATAATATGCTCCCTCTCTCTCCCGCAGCAGCATCAATCCAGCATCTCT 302  
QY 4801 TACATGCTCTCATCAGCCATCTCTCTTCTCAACATGGGGTAAACAAAAATCTACTAAT 4860  
DB 303 TACATGCTCTCATCAGCCATCTCTCTTCTCAATATGGGGTAAATTTAAATTTTACTAAT 362  
QY 4861 CAGCTCTTAATTTAAAGCACATATGTTATGCAAGCTAGTTA-----CGTTA 4905  
DB 363 TTGCTCTTACTTCCAGTATTTATATAGTAGACATACATATCTTGTATACAAGCTAGTAA 422  
QY 4906 GGTGTTGTAATTTTCAATGAAGTTATAGCTGTTAGTGAATGTTACATGATGCTAGATTTTG 4965  
DB 423 AGTGCTATAGTTCAGTGAACCTAGGTGATAGGTGATGTTGTTGTTGTTGTTGTTGTTGTTG 482  
QY 4966 AAACAGAAACCTTTATTTTAAACATTTATTTTAAACCTAGGTAAATCAATGTCGTCGC 5025  
DB 483 CTATGACTACATCCCA-CTAAGATTATTCATACATTAAACCTAGGTAAATGCTGCGA 541  
QY 5026 CAACAGCAACAACTTA 5041  
DB 542 TGAACCTACAGATTTA 557

RESULT 9  
AI992862  
LOCUS AI992862 503 bp mRNA linear EST 08-SEP-1999  
DEFINITION AI992862 701493815 A. thaliana, Ohio State clone set Arabidopsis thaliana  
cDNA clone 701493815, mRNA sequence.  
ACCESSION AI992862  
VERSION AI992862.1 GI:5839767  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 503)

REFERENCE  
AUTHORS Chen, J., Moniyama, M., Chan, B., Mooney, M., Carroon, B., Gilliland, D.,  
Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,  
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D.,  
Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C.,  
Carpio, T., Policky, J., Suzuki, G., Argentin, C., Shah, S.,  
Nobrega, A., Murre, L., Turner, C., Krikorian, S., Elder, L. and  
Hanson, D.

TITLE Arabidopsis thaliana Gene Expression MicroArray  
JOURNAL Unpublished (1999)  
COMMENT Contact: David Smoller, Ph.D.  
Genome Systems, Inc., a wholly owned subsidiary of Incyte  
Pharmaceuticals, Inc.  
4633 World Parkway Circle, St. Louis, MO 63134, USA  
Tel: 877-577-2733  
Fax: 314-427-3324  
Email: service@genomesystems.com.

FEATURES  
source  
1..503  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/db\_xref="taxon:3702"  
/clone="701493815"  
/note="cDNA library was made from selected clones from the  
Arabidopsis thaliana Ohio State clone set."

ORIGIN  
Query Match 3.0%; Score 160.2; DB 9; Length 503;  
Best Local Similarity 63.0%; Pred. No. 3.6e-11;  
Matches 244; Conservative 0; Mismatches 136; Indels 7; Gaps 3;  
QY 1711 AAGAAAACCTTCTTAATGGTTCATACAAAGCTGAGCTCTCTTATATCTCTTG 1770  
DB 1 AAGAAAACCTTCTTAATGGTTCATACAAAGCTGAGCTCTCTTATATCTCTTG 60  
QY 1771 TAGTTCTTATGGGGCTTTGTTTCTTGTGTTCTTTAGAGTAAGAAGTTCTTAAA 1830  
DB 61 TAGTTCTTATGGGGCTTTGTTTCTTGTGTTCTTTAGAGTAAGAAGTTCTTAAA 120  
QY 1831 AAAGATCAAAATGGGAAGGGTAGGCTTCAATTGAAGAGATAGAGAAAGATCAAT 1890  
DB 121 AAAGATCAAAATGGGAAGGGTAGGCTTCAATTGAAGAGATAGAGAAAGATCAAT 177  
QY 1891 AGACAAGTGACATCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCT 1950  
DB 178 TGGCAAGTGACATCTTCGAAAAGAGAA--TGGTCTTTTGAAGAA--TCTTAAACCTCT 233  
QY 1951 GTTCTCTGTGATGCTGAAGTTGCTTGTGTTCTCTCCATAGGGGAAGCTCTCGAA 2010  
DB 234 TTTTCTTTAGGGGAAAATGACCTTTTGGGGCTCCCCCAAGGGGAAACCTCGGGGA 293  
QY 2011 TACTCCACTGATCTTGTGTAACCTTCACTAATCTTCTTACTTTTAAAAAACTTTTAA 2070  
DB 294 AANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 353  
QY 2071 TGCTACTTTATATAGTTTTCCTCC 2097  
DB 354 CGCGGAGAAAAAAGTTTTCCTCC 380

RESULT 10  
BZ004972  
LOCUS oel76b05.g1 B.oleracea002 Brassica oleracea genomic, genomic survey  
DEFINITION sequence.  
ACCESSION BZ004972  
VERSION BZ004972.1 GI:23553230  
KEYWORDS GSS.

ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 694)

REFERENCE  
AUTHORS Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,  
Nash, W., Rabinowicz, P.D. and Wilson, R.K.  
Whole genome shotgun reads from Brassica oleracea  
Unpublished (2002)  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@watson.wustl.edu  
Place: oel76 row: b column: 05  
Seq primer: -28RPOT reverse  
Class: shotgun  
High quality sequence start: 38  
High quality sequence stop: 551.  
Location/Qualifiers  
1..694  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3712"  
/clone\_lib="B.oleracea002"  
/note="Vector: pOTw13; Whole genome shotgun library from  
flowering buds. DNA was purified from a crude nuclear  
prep using Brassica oleracea T0100DH3 buds provided by  
Thomas Osborn at the University of Wisconsin. Genomic  
DNA was provided by Pablo Rabinowicz (CSHL) and the  
shotgun library prepared at Washington University Genome  
Sequencing Center."

ORIGIN  
Query Match 2.8%; Score 150.2; DB 28; Length 694;  
Best Local Similarity 74.9%; Pred. No. 5.4e-10;  
Matches 188; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
QY 1826 TTAAAAAGGATCAAAATGGGAAGGGTAGGTTCAATTGAAGAGGATAGAGAAAGAGA 1885  
DB 181 TTTGAAGAGAAGAGAGATGGGAAGGGTAGGTTCAAGAGAGGATAGAGAAAGAGA 240  
QY 1886 TCAATAGACAAGTGACATCTTCGAAAAGAGAGCTGTTTGAAGAAAGCTCATGAGA 1945  
DB 241 TCAATAGACAAGTTACTTTCTCAAGAGAAGCTGTTGTTGCTCAAGAAAGCTCAAGA 300  
QY 1946 TCTCTGTTCTCTGTGATGCTGAAGTTGCTTGTGTTGTTCTCTCCCATAGGGGAACTCT 2005  
DB 301 TCTCTGTTCTCTGCGATGCTGAGGTTGCTCTCATGCTCTTCTTCCAAAGCGAAGCTCT 360  
QY 2006 TCGAATATCCACATGATCTTGGTAACCTCAACTAATCTTACTTTTAAAAAAATCTTT 2065  
DB 361 TCGAATATCCACAGACTCTTGGTAATATATATATTTTATTTAACTCATAACTATATA 420  
QY 2066 TAATCTGCTAC 2076  
DB 421 TTATAAGTTAC 431

RESULT 11  
CC946428  
LOCUS BOIFJ10TF BO.1.4.1.6\_KB\_nuc Brassica oleracea genomic clone  
DEFINITION BOIFJ10, genomic survey sequence.  
ACCESSION CC946428  
VERSION CC946428.1 GI:33779294  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 813)

**AUTHORS** Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
**TITLE** Whole genome shotgun sequencing of Brassica oleracea  
**JOURNAL** Unpublished (2001)  
**COMMENT** Other GSSs: BOIFJ10TR  
 Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: IF  
 Class: sheared ends.

**FEATURES**

source  
 1. .813  
 Location/Qualifiers  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOIFJ10"  
 /clone\_lib="BO 1.4 1.6 KB nuc"  
 /notes="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared  
 nuclear DNA inserted into PHOS2 using BstXI linkers"

**ORIGIN**

Query Match 2.8%; Score 148.8; DB 29; Length 813;  
 Best Local Similarity 80.6%; Pred. No. 7.3e-10;  
 Matches 174; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 QY 1818 GAAGTTCTTAAAGGATCAAAATGGAGGGGTGAGGTTCAATTGAAGAGGATAGA 1877  
 DB 7 GAGCTTTTGGAGGGAGATACAGAGATGGAGGGGTAGGTTGAGTGGAGAGGATAGA 66  
 QY 1878 GAACAAGATCAATAGACAAGTGCATCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGC 1937  
 DB 67 AAACAAGATCAATAGACAAGTGCATCTCGAAAAGAGAGCTGGTCTTTGAGTGGAGAGC 126  
 QY 1938 TCATGAGATCTGTTCTCTGTGATGCTGAAGTTGCTCTTTGTTGTTCTTCCCATGAGG 1997  
 DB 127 TCATGAGATCTGTTCTCTGTGATGCTGAAGTTGCTCTTTGTTGTTCTTCCCATGAGG 186  
 QY 1998 GAACTCTTCGATCTCCACTGATCTTGGTAACT 2033  
 DB 187 CAAACTCTCAAATATTCACCGACTCTGGTAAT 222

**RESULT 12**

BZ484352 811 bp DNA linear GSS 13-DEC-2002  
 LOCUS BONOZ14TR BO 1.62 KB tot Brassica oleracea genomic clone BONOZ14,  
 DEFINITION genomic survey sequence.

**ACCESSION**

VERSION BZ484352.1 GI:26786750

**KEYWORDS**

SOURCE Brassica oleracea

**ORGANISM**

Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

**REFERENCE**

1 (bases 1 to 811)  
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
**AUTHORS** Whole genome shotgun sequencing of Brassica oleracea  
**TITLE** Unpublished (2001)  
**JOURNAL** Other GSSs: BONOZ14TF  
**COMMENT** Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.

**FEATURES**

source  
 1. .811  
 Location/Qualifiers  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BONOZ14"  
 /clone\_lib="BO 1.6 2 KB tot"  
 /note="Vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared  
 total DNA inserted into PHOS1 using BstXI linkers"

**ORIGIN**

Query Match 2.8%; Score 148; DB 28; Length 811;  
 Best Local Similarity 59.2%; Pred. No. 9.2e-10;  
 Matches 457; Conservative 0; Mismatches 215; Indels 100; Gaps 8;  
 QY 4189 ATGCTTTCTAAACAGGTAACATGTCATCTTCTCTTTC-ATCAACATGTTGTCATT 4247  
 DB 1 ATGCTTTCTAAACAGGTAACATGTCATCTTCTCTTTC-ATCAACATGTTGTCATT 60  
 QY 4248 GCATTAAGTCTTACCTTCCACTGTTCTGCTCCACATTCAGCCCAAGCTATACCT----- 4301  
 DB 61 ACATTAATATTAGCTTCTACTGTTTACTCCACATTCAGGCCAAGCTATTCCTACGACA 120  
 QY 4302 ACGATATCTCATATCTCCACTTAACCTCGGCACCAATTAATAAATAAGAAATCTTTG 4361  
 DB 121 ACGAAATCTTCATTTCTACATTTAGCTTCGACACCAATGATAGAAAATAGTTGATTAC 180  
 QY 4362 CAAATTTGTT-----TGAATAGCATAGATGTTGCTATTGTAATTGA 4402  
 DB 181 ATAGTCTATTGATTGATATCATCATCAGCGCGCTGTACATAGATGGCTTTGCCCATTTA 240  
 QY 4403 TATAATCACCAGCTGTAGTAGATGTTTGTCCGTTAGTTTAAAGTGTTCTCTCG 4462  
 DB 241 GTTTTAAAGTTGCTTCTCAGATTGAAAACCTCGTACCTCTCATCTTATTCTACTGCTCA 300  
 QY 4463 ATTGAAAATATTGTAATCTTTTGAATGTTTGTGCCCATCTTCTTACTTAGTCTCATAT 4522  
 DB 301 TCTATATAGGATGATGAGAAATAGTCTAGCAGTACTAATTAATAAATAATTAAGTCCAAT 360  
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 DB 361 TTTTGGAGCAGTTAAATAATAGTTTGGATAGATATATTTAATAAATGCAATAATAGTA 420  
 QY 4572 GTTCATGTGATGAGTGCACCTGTGAA-----AATTAATCTATTGTAACCA 4615  
 DB 421 GTTTATTGATGAGTGCAGGAACTAGGTGTAAACCAAGATCAAAATGTAGTTACATCTG 480  
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 DB 481 ATGCACATATCTATTGATTAATGAAGTGTGCTCGCTCGAAAATGATGATGATGATGAT 540  
 QY 4657 -TAATATGTTTGAATAATAATTTG-----CTGGCAGAT 4688  
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 DB 601 CAAGGAGAGGAAAAAAGGTTCTTATGGCACAACAAGAGCAATGGGACCAAGAACCATGG 660  
 QY 4749 CCACATATGCTCCCTCTCGCCAGCAGCAGCACCACCAATCCAGCATCTTACATGCT 4808  
 DB 661 CCAAAATATGCTTTCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 720  
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 DB 721 CTCTCATCGCCCATCTCTTTTCTCAACATGGGGTAACTTAAATTTACTAAT 772

**RESULT 13**

T42418  
 LOCUS T42418  
 DEFINITION 5681 Lambda-PRU2 Arabidopsis thaliana cDNA clone 113F9T7, mRNA  
 476 bp mRNA linear EST 07-JAN-1998

sequence.  
 ACCESSION T42418  
 VERSION T42418.1 GI:933190  
 EST  
 KEYWORDS Arabidopsis thaliana (thale cress)  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (bases 1 to 476)  
 REFERENCE Newman,T.; deRuijn,F.J.; Green,P.; Keegstra,K.; Kende,H.;  
 Mcintosh,L.; Ohlrogge,J.; Raikhel,N.; Somerville,S.; Thomasow,M.,  
 Retzel,E. and Somerville,C.  
 AUTHORS Genes galore: a summary of methods for accessing results from  
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 Plant Physiol. 106, 1241-1255 (1994)  
 JOURNAL 95148729  
 MEDLINE  
 PUBLISHED 7846151  
 COMMENT On Nov 29, 1993 this sequence version replaced gi:635006.  
 Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.  
 Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313tcn@bm.cl.msu.edu  
 Seq primer: 17.

## FEATURES

Location/Qualifiers  
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 /strain="var columbia"  
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 /note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not;  
 Lambda PRL2 is a cDNA library derived from equal  
 quantities of 4 pools of mRNA. The mRNA sources were 1) 7  
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 grown roots; 3) staged plants half with 24 hour light  
 cycle, half on 16 hr light, 8 hour dark- rosettes; 4)  
 same plants as 3 but aerial tissue (stems, flowers and  
 siliques. The vector is BRL's lambda Zip-Lox. The cDNA  
 inserts were directionally cloned with Sal-Not arms using  
 oligo dT primed cDNA."

## ORIGIN

Query Match 2.7%; Score 147; DB 14; Length 476;  
 Best Local Similarity 98.7%; Pred. No. 1.8e-09;  
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 DB 1 AACAGATCAATAGACAGTGACATTCGAAAGAGAGAGCTGCTTTTGAAGAAAGCT 60  
 QY 1939 CATGAGATCTCTGTTCTGTGATGCTGAACTTGTCTTGTGTTCTTCCCAAGAGGG 1998  
 DB 61 CATGAGATCTCTGTTCTGTGATGCTGAACTTGTCTTGTGTTCTTCCCAAGAGGG 120  
 QY 1999 AAATCTTCGAATACCTCCAGTATCTTG 2027  
 DB 121 AAATCTTCGAATACCTCCAGTATCTTG 149

## RESULT 14

BG456966  
 LOCUS BG456966 658 bp mRNA linear EST 19-MAR-2001  
 DEFINITION NF098009PL1F1076 Phosphate starved leaf Medicago truncatula cDNA  
 clone NF098009PL 5', mRNA sequence.  
 ACCESSION BG456966  
 VERSION BG456966.1 GI:13380291  
 KEYWORDS EST.

## SOURCE

Medicago truncatula (barrel medic)  
 Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

## REFERENCE

1 (bases 1 to 658)

## AUTHORS

Liu,J.,Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Inman,J.T., Weiler,J.W., May,G.D. and Harrison,M.J.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula phosphate-starved leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Harrison MJ

## TITLE

## JOURNAL

## COMMENT

Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7325  
 Fax: 580 221 7380  
 Email: mjharrison@noble.org  
 Insert Length: 658 Std Error: 0.00  
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Location/Qualifiers

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/dev\_stage="trifoliolate"

/clone\_lib="Phosphate starved leaf"

/note="Vector: Lambda Zap; At the trifoliolate stage, M.

truncatula plants were transplanted to phosphate-free sand

and grown for a further 30 days. During this 30 day

period, the plants were fertilized twice weekly with 1/2

Hoaglands solution containing only 20uM potassium

phosphate. RNA was prepared from above ground tissues."

## ORIGIN

Query Match 2.7%; Score 145.2; DB 12; Length 658;  
 Best Local Similarity 72.1%; Pred. No. 2.4e-09;  
 Matches 189; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
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 QY 1942 GAGATCTCTGTTCTGTGATGCTGAAGTTCCTCTTGTGTTCTTCCCAAGAGGGAAA 2001  
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## RESULT 15

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 DEFINITION NF089C12PL1F1098 Phosphate starved leaf Medicago truncatula cDNA  
 clone NF089C12PL 5', mRNA sequence.  
 ACCESSION B1263356  
 VERSION B1263356.1 GI:14864514  
 KEYWORDS EST.  
 SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.  
 REFERENCE 1 (bases 1 to 665)  
 AUTHORS Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
 Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula phosphate-starved leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Harrison, M.J.  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7325  
 Fax: 580 221 7380  
 Email: mjharrison@noble.org  
 Insert length: 665 Std Error: 0.00  
 Plate: 089 row: C column: 12  
 Seq primer: TCACACAGAAACAGCTATGAC.  
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 truncatula plants were transplanted to phosphate-free sand  
 and grown for a further 30 days. During this 30 day  
 period, the plants were fertilized twice weekly with 1/2  
 Hoaglands solution containing only 20uM potassium  
 phosphate. RNA was prepared from above ground tissues."

ORIGIN  
 Query Match 2.7%; Score 145.2; DB 12; Length 665;  
 Best Local Similarity 72.1%; Pred. No. 2.4e-09;  
 Matches 189; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
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 QY 202 TTTCATTTCCAAACAAAAATAATGGGAGGGGAAGAGTGCAGTTGAAGAGGATTGAGAAC 261  
 DB |||||  
 QY 1882 AAGATCAATAGACAAGTGACATTCTCGAAAGAGAGAGTGGTCTTTTGAAGAAAGCTCAT 1941  
 DB |||||  
 QY 262 AAGTCAATAGACAAGTCACTTTTCAAGNAGAAGGCTCGTTTGTGAGAGAGCACAA 321  
 DB |||||  
 QY 1942 GAGATCTCTGTTCTGTGATGCTGAAGTTGCTCTTGTGTCCTCCCATAGGGGAAA 2001  
 DB |||||  
 QY 322 GAGATCTCTGTTCTGTGATGCTGAAGTTGCTCTCATTTTCTCTACTAAGGCAAG 381  
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 QY 2002 CTCTTCAATCTCCACTGATCTTGGTAACTTCAACTTCTTACTTTTAAAAAAT 2061  
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 QY 382 CTTTGTGAATCTCCAGCATCCTTGGTACGTTTCTTCTTCATATATATAGTTTATT 441  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
9082.245 Million cell updates/sec

Title: US-09-869-582-12

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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6	390.4	7.3	2185	3	US-09-149-976-19
7	303.8	5.7	1054	2	US-08-576-156-1
8	303.8	5.7	1057	3	US-08-659-188-1
9	303.8	5.7	1057	3	US-08-655-227-1
10	303.8	5.7	1057	3	US-08-655-241-1
11	303.8	5.7	1057	4	US-09-398-326-1
12	285.8	5.3	1215	1	US-08-592-214A-1
13	285.8	5.3	1215	3	US-09-149-976-1
14	209.2	3.9	4816	1	US-08-592-214A-22
15	209.2	3.9	4816	3	US-09-149-976-22
16	188.2	3.5	794	1	US-08-592-214A-3
17	188.2	3.5	794	3	US-08-659-188-3
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## ALIGNMENTS

RESULT 1  
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; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
; TITLE OF INVENTION: Genes and Methods of Using Same  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,214A  
; FILING DATE: 26-JAN-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1927  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4379 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2095..2098  
; OTHER INFORMATION: /note= "N = one or more  
; OTHER INFORMATION: nucleotides."  
; FEATURE:  
; NAME/KEY: misc feature  
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RESULT 2

US-09-149-976-17  
 ; Sequence 17, Application US/09149976  
 ; Patent No. 6127123  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanofsky, Martin F.  
 ; TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell & Fiore LLP  
 ; CITY: San Diego  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/149,976  
 ; FILING DATE: 09-SEP-1998  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/592,214  
 ; FILING DATE: 26-JAN-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-UD 3291  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4379 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: 2095..2098  
 ; OTHER INFORMATION: /note= "N = one or more  
 ; OTHER INFORMATION: nucleotides."  
 ; NAME/KEY: misc feature  
 ; LOCATION: 1..4379  
 ; OTHER INFORMATION: /note= "sequence = Arabidopsis  
 ; OTHER INFORMATION: thaliana API gene"  
 US-09-149-976-17

Query Match 58.6%; Score 3148.2; DB 3; Length 4379;  
 Best Local Similarity 80.1%; Pred. No. 0;  
 Matches 4301; Conservative 0; Mismatches 7; Indels 1061; Gaps 9;

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 QY 1 GAATTCGCCGATCTCCATATACATATACATATATATATATATATATATATATATATCT 60  
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Db	1078	TCGATCTTCTCTCTTTTCTTAAATCTCGGTACA	AAATCCGTCGAGCGCAATACATTACAC	1137
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Db 2604 TTTTAAAGTAAGTTAAATTTCAATGCTATTTGAAATTCAGGCATTAATCTTTGGGGAAGA 2663  
Qy 3720 CTTGCAAGCAATGAGCCCTTAAGAGCTTCAGAACTGCGAGCAGCAGCTGACACTCTCT 3779  
Db 2664 CTTGCAAGCAATGAGCCCTTAAGAGCTTCAGAACTGCGAGCAGCAGCTGACACTCTCT 2723  
Qy 3780 TAAGCACATCCGCACTAGAAAAGTATTCCTCTATTTCTGCTATTTCTGTAACATATCTATATA 3839  
Db 2724 TAAGCACATCCGCACTAGAAAAGTATTCCTCTATTTCTGCTATTTCTGTAACATATCTATATA 2783  
Qy 3840 ACTTAAACGTTTACAGTGTATTATTAATGTGAACATTTGAAATAATATGCTGTATGTATC 3899  
Db 2784 ACTTAAACGTTTACAGTGTATTATTAATGTGAACATTTGAAATAATATGCTGTATGTATC 2843  
Qy 3900 AATATATATATCAGTAATCAATTTTATATGATGCTATAGGTTGGTTCGAATGTATG 3959  
Db 2844 AATATATATATCAGTAATCAATTTTATATGATGCTATAGGTTGGTTCGAATGTATG 2903  
Qy 3960 AGTTATGTTGTATTTTAAAGACTCCATTTACTTTAAAGTAAATGGTTGTTTAAATGTTGAT 4019  
Db 2904 AGTTATGTTGTATTTTAAAGACTCCATTTACTTTAAAGTAAATGGTTGTTTAAATGTTGAT 2963  
Qy 4020 GTGTGTATGCGAAGCAACATTTATGTAGAGTCCATCAATGAGCTCCAAAAAAGGTAT 4079  
Db 2964 GTGTGTATGCGAAGCAACATTTATGTAGAGTCCATCAATGAGCTCCAAAAAAGGTAT 3023  
Qy 4080 GTAAAAACCCCTATCAAAATGTATGTTTATAGAGAAACGTTATAGGAAGCTTAATTAACAT 4139  
Db 3024 GTAAAAACCCCTATCAAAATGTATGTTTATAGAGAAACGTTATAGGAAGCTTAATTAACAT 3083  
Qy 4140 CGTCCGTTTCGGAAATGACAGAGGAGGCCATACAGAGCAAAACAGCATGCTTTCTAA 4199  
Db 3084 CGTCCGTTTCGG - AATGACAGAGAGAGGCCATACAGAGCAAAACAGCATGCTTTCTAA 3142  
Qy 4200 ACAGTAACATGTCATCATTTCTTTTCAACAATGTTGTCATTTGCAATTTACTGTTA 4259  
Db 3143 ACAGG - AACACATGTCATCATTTCTTTTCAACAATGTTGTCATTTGCAATTTACTGTTA 3201  
Qy 4260 CTTTCCACTGTTCTGCCACACTTCCAGCCCAAGCTATACCTAGCATCTTTCATATCTC 4319  
Db 3202 CTTTCCACTGTTCTGCCACACTTCCAGCCCAAGCTATACCTAGCATCTTTCATATCTC 3261  
Qy 4320 CACTTAACTTCGGCAACCATTTAAATTAATAAGAAAATCTTTGCAAAATTTGTTGAAATAG 4379  
Db 3262 CACTTAACTTCGGCAACCATTTAAATTAATAAGAAAATCTTTGCAAAATTTGTTGAAATAG 3321  
Qy 4380 CATAGATGTTCTCTATTGATTGATATAATCACCAGCCCTGTACGTAGATATGGTTTGTCCG 4439  
Db 3322 CATAGATGTTCTCTATTGATTGATATAATCACCAGCCCTGTACGTAGATATGGTTTGTCCG 3381  
Qy 4440 TTTAGTTTAAAGTGTCTCTCGGATTGAAAATATTTTGAATCTTTTGAATGTTTGTCC 4499  
Db 3382 TTTAGTTTAAAGTGTCTCTCGGATTGAAAATATTTTGAATCTTTTGAATGTTTGTCC 3441  
Qy 4500 CATCATCTTACTTAGCTCATATCTATGTATATGAATATAGACACTACTCCTAATATATA 4559  
Db 3442 CATCATCTTACTTAGCTCATATCTATGTATATGAATATAGACACTACTCCTAATATATA 3501  
Qy 4560 AATGTTATATAGTTTCAATGTCATGAGTCAACTGTGAAATAAATTAATTTGTAACCATTCG 4619  
Db 3502 AATGTTATATAGTTTCAATGTCATGAGTCAACTGTGAAATAAATTAATTTGTAACCATTCG 3561



Db 509 GTGATTTTATGTTGGATATATAAAGATCAATCACTGATAGATGT-ATGACTTTTATA 567  
 Qy 3978 AGAGCTCCATATCTTAAGTAATGGGTTGTAATGTTGATGTTGTTGATGCGAACC 4037  
 Db 568 AAGAATTAAGTATATAGAGTATGATTAAGTCAATGTAATGGTATGCTTTATGCGAACC 627  
 Qy 4038 AACTTATGTACAGTCCATCAATGAGTCCAAAAAAGGTATGTAAGAACCCCTTATCAAT 4097  
 Db 628 AACTTATGTACAGTCCATCAATGAGTCCAAAAAAGGTATGTAAGAACCCCTTATCAAT 687  
 Qy 4098 STATGCTCTTATAGAGAAAGTATAGAAA-----GCTAATTAACAACTCGTGCG 4146  
 Db 688 TGACGTTTACATAGAAATAACTCGGTGTAAGAACTCTATAGGGAGTCAACAACTCGTGCG 747  
 Qy 4147 TTTCCGAATGACAGAGAGGCCATACAGGAGCAAAACAGCATGCTTTCTTAAACAGGTA 4206  
 Db 748 TTTTCCGAATGACAGAGAGGCCATACAGGAGCAAAACAGCATGCTTTCTTAAACAGGTA 807  
 Qy 4207 ACACATGTCACTATTTCTCTTTCATCAACATGTTGTCATTCATTTACTGTTACCTTCA 4266  
 Db 808 CCAATTTGTCATTTATTTTATATCGTCAAAAGTCTTCTATTTAGTACTGTTAGCTTCA 867  
 Qy 4267 CTGTTCTGTCACATCTCCAGCCAGGTATACCTACGATATCTTCATATCTCCACTTAA 4326  
 Db 868 CTGTTCTACTCCACACTTCCAGCCAGGTATACCTACCTACGATACGAGATTTCTCCACA 927  
 Qy 4327 CTTGGCCACCAATTAATAAATAAGAAATCTTTCGAAATTTGTTGAAATAGCATAGAT 4386  
 Db 928 TATTTCTCAGTCTCGGCACCACTATAACT-AAAATATAGATAAAATATCATTTTT 986  
 Qy 4387 GTTGTCTATTGATTAATTAATCAACAGCCTGCTAGCTAGATATG-GTTTGTCCGTTTATG 4445  
 Db 987 ATAGTCTA-TGATTCATATCTCGTCAGCCAGTACGTAGTTGGGTATTTGCCGTTTATG 1045  
 Qy 4446 TTTAAGGTCTCTCGATGTAAGAAATATTTTGAATCTTTTGAATGTTTGTCCCATCAT 4505  
 Db 1046 TTTAAGGTCTTTTCCGATGTAAGAAATATTTNNNNNACCTACCTTTGATGCTATTAAT 1105  
 Qy 4506 TCTTACTTAGCTCATATCTATGATATGAATATAGACACTACTCTTAATTAATAATGTT 4565  
 Db 1106 GTATATCTATTAGAGTCTGGCTTTTGAATAATGATGATATGATGTTATAGTTG 1165  
 Qy 4566 ATAATAGTTTCAATGATGAGTCACTGTGAAATAAATATTGTTAAACCAATTCATATAT 4625  
 Db 1166 GTAACAACTGCTGTGAAATGAACT-----TGCTA 1194  
 Qy 4626 ATAGTTCTTCACTTTGAAATTTGATGATGATAATATGTTTGAATAAATTTGCTGCA 4685  
 Db 1195 -----TGCTA 1199  
 Qy 4686 GATCAAGAGAGGAGGAAAAATTTCTTAGGGCTCAACAGGAGCAGTGGATCAGCAGAACCA 4745  
 Db 1200 GATTAAGAGAGGAGGAAAGCTTTTAGGGCGCAACAGAGCAATGGGACGAGCAGAACCA 1259  
 Qy 4746 AGGCACCAATATGCTCCCTCTGCTCCACCGCAGCAGCACCAGAAATCCAGCATCTTACAT 4805  
 Db 1260 TGGCCA-TATATGCTCTCCCTCCACCCCGCAGCAGCATCAATCCAGCATCTTACAT 1318  
 Qy 4806 GCTCTCTCATGACCATCTCTTTTCTCAAGTGGGTAAACAAAAATTAATCAATCAGTC 4865  
 Db 1319 GCTCTCTCATGACCATCTCTTTTCTCAACATGGGTAGTTTAAATAATTCGTTCTCT- 1374  
 Qy 4866 TTAATTTAAAGCACATATGTTATGCAAGCTAGTTAGGTGTTGTAATTTCAATGAA 4925  
 Db 1375 CTTACTTTCAAGTCATATGTTATATATACAGATAGTTAGGTGTTATAGTCCAGTGA 1434  
 Qy 4926 GTTATAGCTGTTAGTATGTTTACATGATGCTAGATTTTGAACCTAGAAAACTTTATTTT 4985  
 Db 1435 TTAGGTTGTTAGTATGTTTATGATGCTAGATTTGTAATTTACAACTACTAAGATTTT 1494  
 Qy 4986 AAAACAT-TATTTTATTAACGTAGTTTATGAAATGCTCGCAACAGCAAACTTATTA 5044  
 Db 1495 CAGTTATATAATTAACGTATTGATCATCAATCAATGCTCGTAAAAAACAACAGACTTAT 1554

RESULT 4

US-09-149-976-18  
 ; Sequence 18, Application US/09149976  
 ; Patent No. 6127123  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanofsky, Martin F.  
 ; TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
 ; TITLE OF INVENTION: Genes and Methods of Using Same  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Campbell & Flores LLP  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09149,976  
 ; FILING DATE: 09-SEP-1998  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/592,214  
 ; FILING DATE: 26-JAN-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-UD 3291  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1865 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: 1077..1081  
 ; OTHER INFORMATION: /note="N = one or more  
 ; OTHER INFORMATION: nucleotides."

Qy 5045 GTGTGGAATAATGTACATGGAATGCTTGGAAAAAGCCTAAGTCGACTTTTGTGTTGTTG 5104  
 Db 1555 TTTTGGGAAA--GTAGATGGAATGCTGCTAAAAGCTTAAGAAACCTTTGGGAGCAGGTC 1612  
 Qy 5105 GTCTATG-----TGTTTAAGTACAAATTTAGTTTGTAGATAAATGAAATTAATATATCTT 5160  
 Db 1613 GTATTTATGTTGTTCAATTTAACTTGAGGTAGTTAGATAAATACTATCTTTGATAT 1672  
 Qy 5161 TGACATTTTCAATGAGCATGATTTGATTTTCTTTTGTGTTGACGGTGAACAATATGATT 5220  
 Db 1673 GGCCTTTTACCAATTTCACTTACAAAACATGTGATATTTTTCAGCACC-----TATGT 1722  
 Qy 5221 ACATATGACATTTTCAATATATATATATATATATATATATATATATATATATATATAT 5280  
 Db 1723 AGATATTTTGAAGCTATATATATATATATATATATATATATATATATATATATATAT 1782  
 Qy 5281 AGATGATCCAAATGCGCAATGAGGAGGAATGATCTCGAACTGACTTTGAACCCGTTTACAA 5340  
 Db 1783 AGAAGATCAATGCGCAATGAGGAGGAACGATCTCGATCTGCTCTTTGAACCCGTTTACAA 1842  
 Qy 5341 CTGCAACCTTGGCTG 5355  
 Db 1843 CTGCAACCTTGGCCG 1857





## RESULT 5

US-08-592-214A-19  
Sequence 19, Application US/08592214A  
Patent No. 5811536  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
TITLE OF INVENTION: Genes and Methods of Using Same  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,214A  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1927  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 295..297  
OTHER INFORMATION: /note= "N = one or more  
OTHER INFORMATION: nucleotides."  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 1389..1391  
OTHER INFORMATION: /note= "N = one or more  
OTHER INFORMATION: nucleotides."  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..2185  
OTHER INFORMATION: /note= "sequence = Brassica  
OTHER INFORMATION: oleracea var. botrytis API gene"

US-08-592-214A-19

Query Match 7.3%; Score 390.4; DB 1; Length 2185;  
Best Local Similarity 59.4%; Pred. No. 1.1e-68;  
Matches 1262; Conservative 0; Mismatches 494; Indels 367; Gaps 21;  
QY 3300 TATTATATATAAAATGATATTTGGTTGATGATA--AAGCTAAACCCCTAAATCTGTGAAA 3357  
DB |||||  
DB 353 TAATGATATATATGATCATATAATTTGTTGATGATAGAGCTAGGCCCTAATTTCTGTGAT 412  
QY 3358 TGATCAGTATGAGAGGATCTTTGAACCGCTATGAGAGGTACTCTTTACGCCGGAAGACAGC 3417  
DB |||||  
DB 413 TGAACAGTATGAGAGGATCTTTGAACCGCTATGAGAGGTACTCTTTACGCCGGAAGACAGC 472  
QY 3418 TTATTCACCTGAGCCGAGCTCAATGATTTTCAATAATATTTCTCTCTTTTAAATCCACA 3477  
DB |||||  
DB 473 TTATAGCACCTGAGTCCGAGCTCAATGTAAACCAATTTCTCTCCATTAACTTATATAAAT 532

QY 3478 TATATATATATCAATCTATTGTTAGTATGATGATTTTATTGTTATAAACTTCTGCT 3537  
DB |||||  
DB 533 TAAATATTATTTCAGTATTAGTGATATAT-----ACTTATCTGTATTAAACTTGTGAG 585  
QY 3538 ACACAGACAAACTGGTCGATGGAGTATAACAGGCTTAAGGCTTAAGATTGAGCTTTTGGAG 3597  
DB |||||  
DB 586 ATATAGACGAACTGGTCGATGGAGTATAATAGGCTTAAGGCTTAAGATTGAGCTTTTGGAG 645  
QY 3598 AGAAACGAGAGGTACACATTTTACACTCATCATCTTCTATCTAGAAA-ATCGATCGGTT 3656  
DB |||||  
DB 646 AGAAACGAGAGGTACATTTTCTTATCATCATTTATATATATATGATGAATATCAACAGGAT 705  
QY 3657 CCAT-----TTTAAAGCTAAAGTTAA 3675  
DB |||||  
DB 706 TAAATGTTAGTTAAAAATGCAATGATTTACTTTAATAAAATGATGCAATTTAATAACAAA 765  
QY 3676 AATTCATTGATG--CTATTGAAATTCAGGCAATTTCTTTGGGGAAGACTTTGCAAGCAATGA 3733  
DB |||||  
DB 766 AATGATCGATGCTCTATTGAAATTTAGGCACTATCTTTGGGGAAGACTTTGCAAGCAATGA 825  
QY 3734 GCCCTAAAGAGCTTCAGAACTTGGAGAGCAGCTTGACACTCTCTTAAGACATCCGCA 3793  
DB |||||  
DB 826 GCCCTAAGGAACTCCAGAACTTAGAGCAACAGCTTGTACTCTTAAAGCACTCCGCT 885  
QY 3794 CTAGAAAAGTATTGCTTCTGCTATTTCGTTGAAACATATCTATATAAATCTTAAACGTTTAC 3853  
DB |||||  
DB 886 CTAGAAAAGTATTGAAATCTCTCTATTCTTTAAATTAACATGATATAACAATTAAC----- 939  
QY 3854 AAGTGTATTATAATGTGAACATTTGAAATACATATGTGTATGTATCAATATATATATACAG 3913  
DB |||||  
DB 940 -----ACATATTATTTTATTATTCAAAATACATATATAAATA-GTACATATGTGATTT 992  
QY 3914 TAAATCAATCAATTTGATGATGCTATAGTTGGTTGCGAATGTATGAGTTATGTTGTGTA 3973  
DB |||||  
DB 993 TATTGGTTGGATTTGAAAAGATCAATCACGTCGATTAGAATGTATGACTTTT----- 1044  
QY 3974 TTTTAAAGACTCCATATTACTTTAAAGTAATGGTGTCTTAATGTTGATGTTGTGTATGCGAG 4033  
DB |||||  
DB 1045 -----TAAAGNAATTAGTATATAGAGTATGATTAGTCAATGTAAAGGATGTTATGCGAG 1098  
QY 4034 AACCACCTTATGTACAGTCCATCAATGAGCTCCAAAAAAGAGTATGTAACCCCTATC 4093  
DB |||||  
DB 1099 AACCACCTTATGTACAGTCCATCAATGAGCTCCAAAGAGAGGTATGTATAAACCCCTATC 1158  
QY 4094 AATGTATGCTTATAGAGAACGTTATAGGAA-----GCTAATTAACATCGT 4142  
DB |||||  
DB 1159 AATTTGACGTTTACATAGAAATAACTGCGTGTAAAGAAATCTATAGGGGAGCTAAATAATCGT 1218  
QY 4143 GCCGTTTCGGAATGACAGGAGAGGCGCATACAGGAGCAAAAACAGCATGCTTTCTTAAACA 4202  
DB |||||  
DB 1219 GCCGTTTGGAAATGACAGGAGAGGAGCCATACAGGAAACAAACAGCATGCTTTCCAAGA 1278  
QY 4203 GGTAAACATGTCATCTTCTTTTCATCAACATGTTGTGTCATTTGCAATGCAATGTTTACCT 4262  
DB |||||  
DB 1279 GGTGCAATTTGTCTATTTTATTTCTGCAAAATGTTTCTTATTGTAGATCTGTAGCT 1338  
QY 4263 TCCACTGTTCTGCTCCACACTTCCAGCAAGCTATACCTACGATATCTTCATATCTCCAC 4322  
DB |||||  
DB 1339 TCCACTGTTCT--CACCACTTCAAGCCCAAGCTATACCTAC----- 1378  
QY 4323 TTAACCTCGGCACTTAATAAATAAATAAGAAAAATCTTTGCAAAATTTGTTTGAATAGCAT 4382  
DB |||||  
DB 1379 ----- 1378  
QY 4383 AGATGTTGCTATTGATTGATATAAATACCAGCCTGTACGTAGATATGGTTTGTCCGTTT 4442  
DB |||||  
DB 1379 ----- 1378  
QY 4443 AGTTTAAAGGTCTCTCGGATTGAAATAATTTTGAATCTTTTGAATGTTTGTCCCAT 4502  
DB |||||  
DB 1379 -----CTACGACTAC 1388







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; FILING DATE: 12-21-95
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,336
; FILING DATE: 12-21-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REFERENCE/DOCKET NUMBER: 07251/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1054
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-576-156-1

Query Match 5.7%; Score 303.8; DB 2; Length 1054;
Best Local Similarity 99.3%; Pred. No. 1.5e-51;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 TTCCTAATTGGTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 1780
Db 2 TTTCCTAATTGGTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 61

QY 1781 TTGGGGGCTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAGGATCAA 1840
Db 62 TTGGGGGCTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAGGATCAA 121

QY 1841 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTGA 1900
Db 122 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTGA 181

QY 1901 CATTTCTGAAAAGAGAGCTGGTCTTTGAAGAACTCATGAGATCTCTGTCTCTGTG 1960
Db 182 CATTTCTGAAAAGAGAGCTGGTCTTTGAAGAACTCATGAGATCTCTGTCTCTGTG 241

QY 1961 ATGCTGAAGTGTCTTGTGTTCTCTCCCATAGGGGAACTCTTCGAATACTCCACTG 2020
Db 242 ATGCTGAAGTGTCTTGTGTTCTCTCCCATAGGGGAACTCTTCGAATACTCCACTG 301

QY 2021 ATTCCTG 2027
Db 302 ATTCCTG 308

RESULT 8
US-08-659-188-1
; Sequence 1, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996

```

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; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..893
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1057
; OTHER INFORMATION: /note= "product = Arabidopsis
; OTHER INFORMATION: thaliana APL."
;
US-08-659-188-1

Query Match 5.7%; Score 303.8; DB 3; Length 1057;
Best Local Similarity 99.3%; Pred. No. 1.5e-51;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 TTCTTAATTGGTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 1780
Db 2 TTTCCTAATTGGTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 61

QY 1781 TTGGGGGCTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAGGATCAA 1840
Db 62 TTGGGGGCTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAGGATCAA 121

QY 1841 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTGA 1900
Db 122 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTGA 181

QY 1901 CATTTCTGAAAAGAGAGCTGGTCTTTGAAGAACTCATGAGATCTCTGTCTCTGTG 1960
Db 182 CATTTCTGAAAAGAGAGCTGGTCTTTGAAGAACTCATGAGATCTCTGTCTCTGTG 241

QY 1961 ATGCTGAAGTGTCTTGTGTTCTCTCCCATAGGGGAACTCTTCGAATACTCCACTG 2020
Db 242 ATGCTGAAGTGTCTTGTGTTCTCTCCCATAGGGGAACTCTTCGAATACTCCACTG 301

QY 2021 ATTCCTG 2027
Db 302 ATTCCTG 308

RESULT 9
US-08-655-227-1
; Sequence 1, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PC-DOS/MS-DOS
; FILING DATE: 05-JUN-1996

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RESULT 12  
US-08-592-214A-1  
; Sequence 1, Application US/08592214A  
; Patent No. 5811536

RESULT 13  
US-09-149-976-1  
; Sequence 1, Application US/09149976

Patent No. 6127123  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
TITLE OF INVENTION: Genes and Methods of Using Same  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/149,976  
FILING DATE: 09-SEP-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/592,214  
FILING DATE: 26-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 3291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1215 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(141..905, 909..971, 975..1047)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..1215  
OTHER INFORMATION: /note= "product = Arabidopsis  
OTHER INFORMATION: thaliana APl"  
US-09-149-976-1

Query Match 5.3%; Score 285.8; DB 3; Length 1215;  
Best Local Similarity 99.3%; Pred. No. 6e-48;  
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Qy 1859 TTCAATTGAAGAGGATAGACAAGATCAATAGACAAGTGCACATTTCTCGAAAAAGAGAG 1918  
Db 157 TTCAATTGAAGAGGATAGACAAGATCAATAGACAAGTGCACATTTCTCGAAAAAGAGAG 216  
Qy 1919 CTGCTCTTTTCAAGAAAGCTCATGATCTCTGTCTCTGTGATGCTGAAGTTCCTCTTG 1978  
Db 217 CTGCTCTTTTCAAGAAAGCTCATGATCTCTGTCTCTGTGATGCTGAAGTTCCTCTTG 276  
Qy 1979 TTGCTCTCTCCATAAGGGGAAACTCTTCGAATACTCCACTGATTTCTTG 2027  
Db 277 TTGCTCTCTCCATAAGGGGAAACTCTTCGAATACTCCACTGATTTCTTG 325

RESULT 14  
US-08-592-214A-22  
Sequence 22, Application US/08592214A  
Patent No. 5811536  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
TITLE OF INVENTION: Genes and Methods of Using Same  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,214A  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1927  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4816 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 700..709  
OTHER INFORMATION: /note= "N = one or more  
OTHER INFORMATION: nucleotides."  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 3846..3853  
OTHER INFORMATION: /note= "N = one or more  
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FEATURE:  
NAME/KEY: unsure  
LOCATION: 4545..4548  
OTHER INFORMATION: /note= "N = one or more  
OTHER INFORMATION: nucleotides."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..4816  
OTHER INFORMATION: /note= "sequence = Brassica  
OTHER INFORMATION: oleracea var. botrytis CAL gene"  
US-08-592-214A-22

Query Match 3.9%; Score 209.2; DB 1; Length 4816;  
Best Local Similarity 64.1%; Pred. No. 1.5e-32;  
Matches 400; Conservative 0; Mismatches 208; Indels 16; Gaps 5;  
Qy 1538 ATTAGTACGAGATATACCAATGAGAGTCGACGCAAAATCCTAAAGAAACCACTGTGGT 1597  
Db 742 ATGAAGTCCAGTCAGACCAATGAGAGTCGACGCAAAATCCTAGTAAACTACTCTCTGTT 801  
Qy 1598 TTTTGGAAACAAGAGAAACCACTTTAGCTTTTCCCTAAACCACTCTTACCCA--AATC 1655  
Db 802 TATCCTTGTCCA---AAACCAGCTTTAGGTTTCCCTGAAACCGCTTATCCAAACATCT 858

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; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLESCULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 700..709
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3846..3853
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4545..4548
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4816
; OTHER INFORMATION: /note= "sequence = Brassica
; OTHER INFORMATION: oleracea var. botrytis CAL gene"
; US-09-149-976-22

Query Match 3.9%; Score 209.2; DB 3; Length 4816;
Best Local Similarity 64.1%; Pred. No. 1.5e-32;
Matches 400; Conservative 0; Mismatches 208; Indels 16; Gaps 5;

QY 1538 ATTAGTACGAGATATACCAATGAGAGTCGACACGCAATCTCTTAAAGAACCACTCTGTGGT 1597
Db 742 ATGAAGTCCAGTCAGACCAATGAGAGTCGACACGCAATCTCTTAAAGAACCACTCTGTGGT 801
QY 1598 TTTTGCACCAAGAGAACCACTCTTAAAGAACCACTCTTAAAGAACCACTCTTAAAGAACCACTCT 1655
Db 802 TATCCTTTGTCCA---AAACCACTTTAGGTTTCCCTGAAACCGCTTATTCCTTAAAGAACCACTCT 858
QY 1656 TCTCCATAAATAAGATCCGAGACTCAACACCAAGTCTTTTATTAAGAGAAAGAAAGAA 1715
Db 859 TCTCCTTAAATAAGAGAGACTCTTTCACATGTTATTATCATCAGAGGGAAGAGAGAA 918
QY 1716 AAACCTTCTTAATTTGGTTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTT 1775
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QY 1776 TCTTATTTGGGGTCTTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1835
Db 973 TCTTATTTGGGGTCTTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1032
QY 1836 ---ATCAAAAATGGGAAGGGGTAGGGTTCATTTGAAGAGAGATAGAGAACCAAGATCAATAG 1892
Db 1033 TCTACGAGAAATGGGAAGGGGTAGGGTTCATTTGAAGAGAGATAGAGAACCAAGATCAATAG 1092
QY 1893 ACAAGTGACATTTCTGAAAGAGAGAGTGGTCTTTTGAAGAGAGAGTCTGATGATCTCTGT 1952
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QY 1953 TCTCTGTGATGCTGAAGTTGCTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 2012
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QY 2071 TGTCTATTTATAGTTTCTTTTCCCTTAAAGTGTGATCTTCTTAAATTTATTC 2130
Db 1273 CGCCCTTAAATAAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1332

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RESULT 15
US-09-149-976-22
; Sequence 22, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

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; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLESCULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 700..709
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3846..3853
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4545..4548
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4816
; OTHER INFORMATION: /note= "sequence = Brassica
; OTHER INFORMATION: oleracea var. botrytis CAL gene"
; US-09-149-976-22

Query Match 3.9%; Score 209.2; DB 3; Length 4816;
Best Local Similarity 64.1%; Pred. No. 1.5e-32;
Matches 400; Conservative 0; Mismatches 208; Indels 16; Gaps 5;

QY 1538 ATTAGTACGAGATATACCAATGAGAGTCGACACGCAATCTCTTAAAGAACCACTCTGTGGT 1597
Db 742 ATGAAGTCCAGTCAGACCAATGAGAGTCGACACGCAATCTCTTAAAGAACCACTCTGTGGT 801
QY 1598 TTTTGCACCAAGAGAACCACTCTTAAAGAACCACTCTTAAAGAACCACTCTTAAAGAACCACTCT 1655
Db 802 TATCCTTTGTCCA---AAACCACTTTAGGTTTCCCTGAAACCGCTTATTCCTTAAAGAACCACTCT 858
QY 1656 TCTCCATAAATAAGATCCGAGACTCAACACCAAGTCTTTTATTAAGAGAAAGAAAGAA 1715
Db 859 TCTCCTTAAATAAGAGAGACTCTTTCACATGTTATTATCATCAGAGGGAAGAGAGAA 918
QY 1716 AAACCTTCTTAATTTGGTTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTT 1775
Db 919 AAACCTTCTTAATTTAGATCG-----AGCTTGTCTGTTATCTCTCTTATATAGTTTATAT 972
QY 1776 TCTTATTTGGGGTCTTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1835
Db 973 TCTTATTTGGGGTCTTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1032
QY 1836 ---ATCAAAAATGGGAAGGGGTAGGGTTCATTTGAAGAGAGATAGAGAACCAAGATCAATAG 1892
Db 1033 TCTACGAGAAATGGGAAGGGGTAGGGTTCATTTGAAGAGAGATAGAGAACCAAGATCAATAG 1092
QY 1893 ACAAGTGACATTTCTGAAAGAGAGAGTGGTCTTTTGAAGAGAGAGTCTGATGATCTCTGT 1952
Db 1093 ACAAGTGACATTTCTGAAAGAGAGAGTGGTCTTTTGAAGAGAGAGTCTGATGATCTCTGT 1152
QY 1953 TCTCTGTGATGCTGAAGTTGCTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 2012
Db 1153 TCTTGTGATGCTGAGGTTTCCCTTATGTTCTCTCCCAAGAGGGAAGAGTCTGAGTA 1212
QY 2013 CTCCTGATTTCTTGTAAGTCTC---AACTAATTTCTTTTACTTTTAAATAAATCTTTTAAATC 2070
Db 1213 CTCCTGATTTCTTGTAAGTCTC---AACTAATTTCTTTTACTTTTAAATAAATCTTTTAAATC 1272
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Qy 2131 ACTACTGCTTTTGTATATATTT 2154  
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Search completed: October 1, 2004, 04:33:58  
Job time : 382 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 17:32:03 ; Search time 1839 Seconds  
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12400.395 Million cell updates/sec

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Perfect score: 5368  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002s:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	3142.6	58.5	4375	2	Aat76892 Arabidops
5	1790.4	33.4	1838	6	Aal42830 Arabidops
6	474.4	8.8	1865	2	Aav58319 Brassica
7	474.4	8.8	1865	3	Aac61416 Genomic D
8	470.4	8.3	1860	2	Aat76893 Brassica
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11	387.8	7.2	2179	2	Aat76894 Cauliflow
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## ALIGNMENTS

RESULT 1  
AAA15015  
ID AAA15015 standard; DNA; 5368 BP.  
XX  
AC AAA15015;  
XX  
DT 21-AUG-2000 (first entry)  
XX  
DE Nucleotide sequence of Arabidopsis AP1 promoter.  
XX  
KW AP1 promoter; transgenic plant; suppressed flowering;  
KW floral organ selective regulatory element; wood; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN W0200023578-A2.  
XX  
PD 27-APR-2000.  
XX  
PF 15-OCT-1999; 99WO-US024407.  
XX  
PR 16-OCT-1998; 98US-0104604P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Yanofsky MF;  
DR WPI; 2000-339680/29.  
XX  
PT Transgenic plants in which flowering is suppressed by a tissue specific  
PT cytotoxic gene product, useful for the production of wood for use as  
PT lumber or pulp.  
XX  
PS Claim 29; Fig 6a-f; 79pp; English.  
XX  
CC The present sequence represents the Arabidopsis AP1 promoter. The  
CC promoter is used to produce transgenic plants of the invention, which are  
CC characterized by suppressed flowering. The plants are transformed with a  
CC construct comprising a floral organ selective regulatory element (e.g.  
CC present sequence), operatively linked to a nucleotide sequence encoding a  
CC cytotoxic gene product (which is inheritable by the progeny). The plants  
CC may be grown for either human consumption or for use as a raw material in  
CC industry. When trees, they are particularly suitable for cultivation to  
CC provide wood. As the flowering process consumes 20-35% of the energy of a  
CC typical plant, it is advantageous to suppress flowering in order to  
CC improve wood and lumber yields. Suppression of flowering may be desired



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 3901 ATATATATCATGATTAATCAATATCAATTTGATGATGCTATAGGTTGGTTGCAATGATGA 3960  
 3901 ATATATATCATGATTAATCAATATCAATTTGATGATGCTATAGGTTGGTTGCAATGATGA 3960  
 3961 GTTATGTTGTTATTTTGAACCTCAATTTTCAATTTAAGTAAATGTTGTTTAAATGTTGATG 4020  
 3961 GTTATGTTGTTATTTTGAACCTCAATTTTCAATTTAAGTAAATGTTGTTTAAATGTTGATG 4020  
 4021 TGTGTGTATGCAAAACCAACTTATGTACGAGTCCATCAATGAGCTCCAAAAAAGGTATG 4080  
 4021 TGTGTGTATGCAAAACCAACTTATGTACGAGTCCATCAATGAGCTCCAAAAAAGGTATG 4080  
 4081 TAAACCCCTATCAAAATGATGCTTTATAGAGAAAGCTATAGGAAAGCTTAATTAACAATC 4140  
 4081 TAAACCCCTATCAAAATGATGCTTTATAGAGAAAGCTATAGGAAAGCTTAATTAACAATC 4140  
 4141 GTGCCGTTTTCGGAATGACAGGAGAGGCTTACAGGACAAACAGCATGCTTTCTTAA 4200  
 4141 GTGCCGTTTTCGGAATGACAGGAGAGGCTTACAGGACAAACAGCATGCTTTCTTAA 4200  
 4201 CAGGTAAACATGTCATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 4260  
 4201 CAGGTAAACATGTCATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 4260

QY 4261 CTTCCACTGTTCTCTCCACATCTTCCAGCCAGCTATACCTACGATATCTTTCATATCTCC 4320  
 Db 4261 CTTCCACTGTTCTCTCCACATCTTCCAGCCAGCTATACCTACGATATCTTTCATATCTCC 4320  
 QY 4321 ACTTAACCTTGGCACCATTAAATAAAAAATAGAAAAATCTTTGCAAAATTTGTTGAAATAGC 4380  
 Db 4321 ACTTAACCTTGGCACCATTAAATAAAAAATAGAAAAATCTTTGCAAAATTTGTTGAAATAGC 4380  
 QY 4381 ATAGATGTTGCTATATGATTAATAATCAACAGCCTGTACGTAGATATGTTGTCGGT 4440  
 Db 4381 ATAGATGTTGCTATATGATTAATAATCAACAGCCTGTACGTAGATATGTTGTCGGT 4440  
 QY 4441 TTAGTTTTAAAGTGTCCTCCGATGGAATAATTTTGAATCTTTTGAATGTTTGTCTCC 4500  
 Db 4441 TTAGTTTTAAAGTGTCCTCCGATGGAATAATTTTGAATCTTTTGAATGTTTGTCTCC 4500  
 QY 4501 ATCAATCTTACTAGCTCATATCTATGTATATGAATATAGACACTACTCTTAATATATA 4560  
 Db 4501 ATCAATCTTACTAGCTCATATCTATGTATATGAATATAGACACTACTCTTAATATATA 4560  
 QY 4561 ATGTTATATATAGTTCAATGCAATGCACTGCAACTGTGAAAAATACATATTTGTAACCATGCA 4620  
 Db 4561 ATGTTATATATAGTTCAATGCAATGCACTGCAACTGTGAAAAATACATATTTGTAACCATGCA 4620  
 QY 4621 TATATATAGTTTCTTCACTTTGAAATTTGATGATGATATATGTTTGAATATATAATTTGC 4680  
 Db 4621 TATATATAGTTTCTTCACTTTGAAATTTGATGATGATATATGTTTGAATATATAATTTGC 4680  
 QY 4681 TGGCAGATCAAGGAGGAGGAAAAATTTCTTAGGGCTCAACGAGCAGTGGGATCAGCAG 4740  
 Db 4681 TGGCAGATCAAGGAGGAGGAAAAATTTCTTAGGGCTCAACGAGCAGTGGGATCAGCAG 4740  
 QY 4741 AACCAAGGCCACATATGCTCCCTCCCTCTGCCACGCGAGCAGCAAAATCCAGCATCCT 4800  
 Db 4741 AACCAAGGCCACATATGCTCCCTCCCTCTGCCACGCGAGCAGCAAAATCCAGCATCCT 4800  
 QY 4801 TACATGCTCTCTCATCAGCCATCTCTTTCTCAACATGGGTAAACAAAAATTAATAAT 4860  
 Db 4801 TACATGCTCTCTCATCAGCCATCTCTTTCTCAACATGGGTAAACAAAAATTAATAAT 4860  
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 Db 4861 CAGTCTTAATTTAAAGCACAATATGTTATGCAAGCTAGTTAGCTAGGTGTTGTAATTTCA 4920  
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 Db 4921 TTGAAGTTATAGCTGTTAGTATGTTTACATGATCTAGATTTTGAACCTAGAAAACTTT 4980  
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 Db 4981 ATTTTAAACATTTATTTTAACTAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTTT 5040  
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 Db 5041 ATTAGTGTGAAAAATGACATGGAATGTTTGCAGAAAGCCCTAAGTCGACTTTTGTGTT 5100  
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 Db 5101 GTTGGCTATGTTTAAAGTACAAATTTAGTTTGTAGTAAATGAAATTAATATATCTT 5160  
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 Db 5161 TGACATTTTCAACATGGAATGATTTTGAATTTTCTTGTGTGACGGTGAACATATGATT 5220  
 QY 5221 ACATATGCACTTTTCAATATATATATATATATATATATATATATATATATATATAT 5280  
 Db 5221 ACATATGCACTTTTCAATATATATATATATATATATATATATATATATATATATAT 5280  
 QY 5281 AGATGATCCCAATGCAATGAGGAGGAATGATCTCGAACTGCTTTGAACCGGTTTACAA 5340  
 Db 5281 AGATGATCCCAATGCAATGAGGAGGAATGATCTCGAACTGCTTTGAACCGGTTTACAA 5340

QY 5341 CTGCAACCTTGGCTGCTTTCGGCGCATGA 5368  
 Db 5341 CTGCAACCTTGGCTGCTTTCGGCGCATGA 5368  
 RESULT 2  
 ID AAV58318 standard; DNA; 4379 BP.  
 XX AAV58318;  
 AC AAV58318;  
 DT 19-NOV-1998 (first entry)  
 XX Arabidopsis thaliana API gene.  
 KW CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;  
 early flowering promotion; angiosperm; API gene; ds.  
 OS Arabidopsis thaliana.  
 PN US811536-A.  
 XX 22-SEP-1998.  
 XX 26-JAN-1996; 96US-00592214.  
 PR 26-JAN-1996; 96US-00592214.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX Yanofsky MF;  
 DR WPI; 1998-530945/45.  
 CC Cloned CAULIFLOWER genes - and vectors for converting shoot meristems to  
 floral meristems.  
 PS Disclosure; Fig 10; 93pp; English.  
 CC This sequence encodes the Arabidopsis thaliana API protein. This sequence  
 was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER  
 (CAL) protein of the invention. An expression vector containing the CAL  
 DNA sequence can be used to convert shoot meristems to floral meristems,  
 especially to promote early flowering in angiosperms  
 SQ Sequence 4379 BP; 1488 A; 706 C; 714 G; 1467 T; 0 U; 4 Other;  
 Query Match 58.6%; Score 3148.2; DB 2; Length 4379;  
 Best Local Similarity 80.1%; Pred. No. 0;  
 Matches 4301; Conservative 0; Mismatches 7; Indels 1061; Gaps 9;  
 QY 1 GAATCCCGGATCCATATACATATACATATATATATATATATATATATATATATATAT 60  
 Db 1 GAATCCCGGATCCATATACATATACATATATATATATATATATATATATATATATAT 60  
 QY 61 ATTTCTCTATACACTATCTTTTAACTTATGATGTTTCAAACTCAGGACGTACATGTT 120  
 Db 61 ATTTCTCTATACACTATCTTTTAACTTATGATGTTTCAAACTCAGGACGTACATGTT 120  
 QY 121 TTAATTTGGTTATATAACCAACGACCAATTTCAAGTATATATATATATATATATATAT 180  
 Db 121 TTAATTTGGTTATATAACCAACGACCAATTTCAAGTATATATATATATATATATATAT 180  
 QY 181 AATATACTTCTATGAAGAAATACATAAAGTTGATTAATAATGCAAGTGACATCTTTT 240  
 Db 181 AATATACTTCTATGAAGAAATACATAAAGTTGATTAATAATGCAAGTGACATCTTTT 240  
 QY 241 AGCATAGTTTCATTTGGCATAGAAATATATACTTAAATAAATGAATTTTAACTTAAATA 300  
 Db 241 AGCATAGTTTCATTTGGCATAGAAATATATACTTAAATAAATGAATTTTAACTTAAATA 300  
 QY 301 GATTTTACTATATATACAAATTTTCTTTTACATGCTCTAAATTTATTTTCTTAAATTTAG 360  
 Db 301 GATTTTACTATATATACAAATTTTCTTTTACATGCTCTAAATTTATTTTCTTAAATTTAG 360

301 GATTTTACTATATACAA-TTTTCTTTTTCATCGTCTAAATTTATTTTCTTAAATATAG 359 Db  
361 TATGATTTGTTGTTTGGATGAACAATAATACCGTAAAGCAATAGTTGCTAAAGAGTGCCA 420 QY  
360 TATGATTTGTTGTTTGGATGAACAATAATACCGTAAAGCAATAGTTGCTAAAGAGTGCCA 419 Db  
421 AATATTTATAAATACAAAGTAAATCAAAATAGGAAGAAGACACGTTGGAAACACCAAT 480 QY  
420 AATATTTATAAATACAAAGTAAATCAAAATAGGAAGAAGACACGTTGGAAACACCAAT 479 Db  
481 AAGAGAAGAAATGGAAAAACAGAAAGAAATTTTAAACAGAAAAATCAATTTAGTCCTC 540 QY  
480 AAGAGAAGAAATGGAAAAACAGAAAGAAATTTTAAACAGAAAAATCAATTTAGTCCTC 539 Db  
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600 GAAATGGTCCAACTTTTCACTTAATATATATTTTCTTAAGGCTTATGCAATATATG 659 Db  
661 CCTTAAGCAAAATGCCAAATCTGTTTTTTTTTTTGTATTGATATTGACTGAAAAATAAG 720 QY  
660 CCTTAAGCAAAATGCCAAATCTGTTTTTTTTTTTGTATTGATATTGACTGAAAAATAAG 719 Db  
721 GGGTTTTTTCACACTTTGAAGATCTCAAAAGAGAAAACTATTACACCGAAATTCATTGTA 780 QY  
720 GGGTTTTTTCACACTTTGAAGATCTCAAAAGAGAAAACTATTACACCGAAATTCATTGTA 779 Db  
781 AAAGAGTGAATTAAGCAAAATTTAGCAAAAGGTTTTTATGTTGTTTATTCATTATATGATT 840 QY  
780 AAAGAGTGAATTAAGCAAAATTTAGCAAAAGGTTTTTATGTTGTTTATTCATTATATGATT 839 Db  
841 GACATCAAAATGTATATATATGTTGTTTATTTAAACAATATATATGGATATAACGTACA 900 QY  
840 GACATCAAAATGTATATATATGTTGTTTATTTTAAACAATATATATGGATATAACGTACA 899 Db  
901 AACTAAATATGTTTGAATGACGAAAAAATAATATGATATGTTTGAATTAACAACATAGCAC 960 QY  
900 AACTAAATATGTTTGAATGACGAAAAAATAATATGATATGTTTGAATTAACAACATAGCAC 959 Db  
961 ATATCAACTGATTTTGTGCTGATCATCTACAACTTAATAAGAACACACACATTTGAAA 1020 QY  
960 ATA-TCAACTGATTTTGTGCTGATCATCTACAACTTAATAAGAACACACACATTTGAAA 1018 Db  
1021 AAATCTTGCACAAATACTATTTTGGGTTTGAATTTTGAATCTTACAAATTTATCTTC 1080 QY  
1019 AAATCTTGCACAAATACTATTTTGGGTTTGAATTTTGAATCTTACAAATTTATCTTC 1077 Db  
1081 TCGATCTTCTCTCTTCTTAAATCTCGGTACAAATCGTTCGACGCAATACATTACAC 1140 QY  
1078 TCGATCTTCTCTCTTCTTAAATCTCGGTACAAATCGTTCGACGCAATACATTACAC 1137 Db  
1141 AGTTGTCATTTGTTCTCAGCTCTACCAAAACATCTATTGCCAAAGAAAGGCTTATTT 1200 QY  
1138 AGTTGTCATTTGTTCTCAGCTCTACCAAAACATCTATTGCCAAAGAAAGGCTTATTT 1197 Db  
1201 GTACTTCACTGTTACAGCTGAGAACATTAATATAATAAGCAAAATTTGATAAACAAAGG 1260 QY  
1198 GTACTTCACTGTTACAGCTGAGAACATTAATATAATAAGCAAAATTTGATAAACAAAGG 1257 Db  
1261 GTTCTCACCTTATTCAAAAAGATAGTGTAAAAATAGGGTAAATAGAGAAATGTTTAAATAAAA 1320 QY  
1258 GTTCTCACCTTATTCAAAAAGATAGTGTAAAAATAGGGTAAATAGAGAAATGTTTAAATAAAA 1317 Db  
1321 GGAATTAANAATAGATATTTTGGTT-GGTTCAAGATTTTGTTCGTAGATCTACAGGAA 1379 QY  
1318 GGAATTAANAATAGATATTTTGGTTGGGTTCAAGATTTTGTTCGTAGATCTACAGGAA 1377 Db  
1380 ATCTCCGCGCTCAATGCAAGCAAGGTGACACTTGGGGAGGACCAAGTGGTCCGTACAA 1439 QY  
1378 ATCTCCGCGCTCAATGCAAGCAAGGTGACACTTGGGGAGGACCAAGTGGT-CGTACAA 1436 Db

1440 TGTACTTACCCATTTCTTTCACGAGAGCTCGAATAACAAATGTTTATTTTCAATTT 1499 QY  
1437 TGTACTTACCCATTTCTTTCACGAGAGCTCGAATAACAAATGTTTATTTTCAATTT 1496 Db  
1500 TTAAGTCCGACGTTTTATTAAAAAATCATGGACCCGACATTAGTAGAGATATACCAATG 1559 QY  
1497 TTAAGTCCGACGTTTTATTAAAAAATCATGGACCCGACATTAGTAGAGATATACCAATG 1556 Db  
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1557 AGAAGTCGACACGCAAAATCCTTAAAGAAACCACTGTGGTTTTTGCAAAACAGAAACCGAG 1616 Db  
1620 CTTTAGCTTTTCCCTTAAACCACTCTTACCCTAAATCTCTCCATAAATAAGATCCCGAGA 1679 QY  
1617 CTTTAGCTTTTCCCTTAAACCACTCTTACCCTAAATCTCTCCATAAATAAGATCCCGAGA 1676 Db  
1680 CTCAAAACACAAGTCTTTTATAAAGGAAAGAAAGAAACTTTTCTTAATTTGGTTCAATACC 1739 QY  
1677 CTCAAAACACAAGTCTTTTATAAAGGAAAGAAAGAAACTTTTCTTAATTTGGTTCAATACC 1736 Db  
1740 AAAAGTCTGAGCTCTTCTTTATATATCTCTTGTAGTTTCTTATTTGGGGGCTTTTGTGTTGT 1799 QY  
1737 AAAAGTCTGAGCTCTTCTTTATATATCTCTTGTAGTTTCTTATTTGGGGGCTTTTGTGTTGT 1796 Db  
1800 TTGGTTCTTTTATAGATGAAGATTTCTTAAAAAGGATCAAAATGGGAGGGTAGGGT 1859 QY  
1797 TTGGTTCTTTTATAGATGAAGATTTCTTAAAAAGGATCAAAATGGGAGGGTAGGGT 1856 Db  
1860 TCAATTTGAAGAGATAGAGAACAAAGATCAATAGACAAAGTGACATCTCCGAAAAGAGAGC 1919 QY  
1857 TCAATTTGAAGAGATAGAGAACAAAGATCAATAGACAAAGTGACATCTCCGAAAAGAGAGC 1916 Db  
1920 TGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGATGCTGAAAGTTGCTCTTGT 1979 QY  
1917 TGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGATGCTGAAAGTTGCTCTTGT 1976 Db  
1980 TGTCTTCTCCATAAGGGGAAACTCTTCCAAATCTCCACTGATTTCTTGGTAACTTCAACT 2039 QY  
1977 TGTCTTCTCCATAAGGGGAAACTCTTCCAAATCTCCACTGATTTCTTGGTAACTTCAACT 2036 Db  
2040 AATCTTTACTTTTAAAAAAATCTTTTAAATCTGCTACTTTATATAGTTTTTTTCCCCCTT 2099 QY  
2037 AATCTTTACTTTTAAAAAAATCTTTTAAATCTGCTACTTTATATAGTTTTTTTCCCC- 2093 Db  
2100 AAGTTGACTACTGATTTGCCCCTAATTTATTCACTACTGCTTTTGTATATATTTTCTAGG 2159 QY  
2094 ----- 2093 Db  
2160 GCTTCCATTTTGGATTTTGTAGTAGCCAGAAAAATGTTTAAATACAAATTTGTATAATT 2219 QY  
2094 ----- 2093 Db  
2220 TAAAAATCAAAACTTTTAGGCGCTAGTGAAGTGAACCTAGAACACACAGATTTATACCAT 2279 QY  
2094 ----- 2093 Db  
2280 AGTAATTTACCTTGATATATTTGTGCAATATTTATCAGCATCATATCTTCAAACTCAAGAGA 2339 QY  
2094 ----- 2093 Db  
2340 TATAGAGGGTATGTTAAATCTTTTGAACACTAGGTTTTTGTATCCCTAACTCAATGAATCCT 2399 QY  
2094 ----- 2093 Db  
2400 TTTGTTCTCCATAGCCATGCTTTTCGAATTTTGACAGATCTAAGCTCTAATTTGATGCCATA 2459 QY  
2094 ----- 2093 Db  
2460 GTAAGAAAAATAGATCTGTAGTTTTTCACTCGCTCACTGAGTTTCGAGTTTTTAAATGAAGTG 2519 QY  
2094 ----- 2093 Db

QY 2520 TCGTTTCCTTTTTCATATATAGTTCGAACCTGGATTATTAATTAATAAATAATTATATGGACGA 2579  
Db 2094 ----- 2093  
QY 2580 GAAAAATAATTTAAAAATAGATATAGATAAACAATGTCAAAATGAGAAATTTTTTATTAGAAAG 2639  
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QY 2640 AATATTAACTTACGAGTTGTTTTTTTTCAGCTGTAAAAGAATATCTAAATTTGTTCTCAC 2699  
Db 2094 ----- 2093  
QY 2700 GACTGTGCTTCATGTTTTTGCAAAATCTAAGCAAGAAAAATGTTTAAACTCGGATCTTAAG 2759  
Db 2094 ----- 2093  
QY 2760 ATTATGAACCTGTAATATAAACAATAATATAGTATTAATAATTTGAACATAGTGTGCTTCTT 2819  
Db 2094 ----- 2093  
QY 2820 TTGCTACTTTGACTTTTAGAAATTAACAACCTGAAACAAGATGTCAAACTCGAGTAGGAGT 2879  
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QY 2880 CTTTGACCTCTGGGATCCATAAAAAAGAACTAACTCCATCCTAAAAATCGGCTTCTTACCG 2939  
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QY 2940 ATGGTCAAACTTAGCTCCAAACAAGCAACAGCTGTTCTTCTTTTCTTTTCTTTTCTTTT 2999  
Db 2094 ----- 2093  
QY 3000 TTTTAAAGCATTTGCTTGTCTGAAABAAAATAAAGATTGGTAATTTGCAAGATTATAAT 3059  
Db 2094 ----- 2093  
QY 3060 AATTATTATTAATGTGCGCACTAAGAGAATTTTCTGTACCTAATTTGTAGCAAAATTAAT 3119  
Db 2094 ----- 2093  
QY 3120 GAAACCGAGTTAGAACTCGAAGCTAAGACATAGGCTATGATTCATACGTGTTTGT 3179  
Db 2094 ----- 2093  
QY 3180 ATTATAAGGTATCATAGAGATCGGTACTTGTATTTGTTATAGGAATCTTGGTTAAATG 3239  
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QY 3240 CATAAAACCATTCATTAGATTTATCCTAAAATGTGATGATATTTTGGTCACATCTCCATAT 3299  
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QY 3300 TATTATTATAAATAAGTAATTTGGTTGATGATAAAGCTAAACCTAATTTCTGTGAATG 3359  
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Db 2304 ATCAGTATGGAGAAGATACTTTGAACGCTATGAGAGTACTCTTAGCCGGAAGACAGCTT 2363  
QY 3420 ATTGCACCTGAGTCCGACGTCATTTGATTTTCATTAATAATTTTCTCTTTTAAATCCACATA 3479  
Db 2364 ATTGCACCTGAGTCCGACGTCATTTGATTTTCAATAAATATTCTCTCTTTTAAATCCACATA 2423  
QY 3480 TATATTATATCAATCTATTTGTAGTATTTGATGAATTTTATTGTTATATAAACTCTGGTAC 3539  
Db 2424 TATATTATATCAATCTATTTGTAGTATTTGATGAATTTTATTGTTATATAAACTCTGGTAC 2483  
QY 3540 ACAGACAAACTGGTTCGATGGAGTATAACAGGCTTAAGGCTAAGATTGAGCTTTTGGAGAG 3599  
Db 2484 ACAGACAAACTGGTTCGATGGGATATAACAGGCTTAAGGCTAAGATTGAGCTTTTGGAGAG 2543  
QY 3600 AAACGAGAGGTACACATTTTACACTCATCACATTTCTATCTAGAAAAATCGATCGGGTTCCA 3659

Db 2544 AAACGAGAGGTACACATTTTACACTCATCACATTTCTATCTAGAAAAATCGATCGGGTTCCA 2603  
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Db 2604 TTTTAAAGTAAGTTAAAAATTCATTGATGCTATTAATAATTCAGGCAATTAATTTGGGGAAGA 2663  
QY 3720 CTTGCAAGCAATGAGCCCTAAAGAGCTTCAAAATTCGAGAGCAGCTTGACACTGCTCT 3779  
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QY 3780 TAAGCACATCCGCACTAGAAAAAGTATTGCCCTTCTGCTAATTTTCGTTGAACATATCTATATA 3839  
Db 2724 TAAGCACATCCGCACTAGAAAAAGTATTGCCCTTCTGCTAATTTTCGTTGAACATATCTATATA 2783  
QY 3840 ACTTAAACGTTTACAAGTGTATTATATGTAACATTTGAACATTTGAATAATATGATGTATATC 3899  
Db 2784 ACTTAAACGTTTACAAGTGTATTATTAATGTAACATTTGAACATTTGAATAATATGATGTATATC 2843  
QY 3900 AATATATATATCAGTAAATCAATTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAAT 3959  
Db 2844 AATATATATATCAGTAAATCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAAT 2903  
QY 3960 AGTTATGTTGTATTTTAAAGCTCCATTTTAAAGTAAATGAGTAAATGAGTAAATGAGTAAATGAGT 4019  
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QY 4020 GTGTGTATGCGAAGCAACTTATGTACGAGTCCATCAATCAATCAATCAATCAATCAATCAATCAAT 4079  
Db 2964 GTGTGTATGCGAAGCAACTTATGTACGAGTCCATCAATCAATCAATCAATCAATCAATCAATCAAT 3023  
QY 4080 GTAAAAACCTTATCAAAATGTATGCTTATAGAGAAACGTATAGGAAACGTATTAACCAAT 4139  
Db 3024 GTAAAAACCTTATCAAAATGTATGCTTATAGAGAAACGTATAGGAAACGTATTAACCAAT 3083  
QY 4140 CGTCCGCTTTCGGAATGACAGAGAGGCGCATACAGGAGCAAAACAGCAGCTTTCTTAA 4199  
Db 3084 CGTCCGCTTTCGCG - AATGACAGAGAGAGGCGCATACAGGAGCAAAACAGCAGCTTTCTTAA 3142  
QY 4200 ACAGGTAAACATGTCAATCAATTTCTTTTCAACATGTTGTCATTTGCAATTTACTGTTA 4259  
Db 3143 ACAGG - AACACATGTCAATTTCTTTTCAACATGTTGTCATTTGCAATTTACTGTTA 3201  
QY 4260 CTTTCCACTGTTCTGCTCCACACTTCCAGCAAGCTATACCTAGCATATCTTCATATCTC 4319  
Db 3202 CTTTCCACTGTTCTGCTCCACACTTCCAGCAAGCTATACCTAGCATATCTTCATATCTC 3261  
QY 4320 CACTTAACTTCGGCACCATTTAAATAAATAAGAAAAATCTTTGCAAAATTTGTTGAAATAG 4379  
Db 3262 CACTTAACTTCGGCACCATTTAAATAAATAAGAAAAATCTTTGCAAAATTTGTTGAAATAG 3321  
QY 4380 CATAGATGTTGTCTATTGATGATATAATCAACAGCCTGTACGATAGATATGTTGTCGG 4439  
Db 3322 CATAGATGTTGTCTATTGATGATATAATCAACAGCCTGTACGATAGATATGTTGTCGG 3381  
QY 4440 TTTAGTTTTAAGGTGCTCTCGGATTCGAAATATTTTGAATCTTTTGAATGTTTGTCC 4499  
Db 3382 TTTAGTTTTAAGGTGCTCTCGGATTCGAAATATTTTGAATCTTTTGAATGTTTGTCC 3441  
QY 4500 CATCAITTTCTTACTTACTGCTCATATCTATGATATGAATATAGACACTACTCTCTAATTTAA 4559  
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Db 3502 AATGTTTAAATAGTTCATTGCTAGTGCACACTGTGAATAATTAACATTTTGAACCAATGC 3561  
QY 4620 ATATATATAGTTTCTTCACTTTTGAATAATGATGATGATAATATGATGATAATGATAATGATA 4679  
Db 3562 ATATATATAGTTTCTTCACTTTTGAATAATGATGATGATAATATGATGATAATGATAATGATA 3621  
QY 4680 CTGCGAGATCAAGGAGAGGAAAAATTTCTTCTAGGGCTCAACAGGAGCAGTGGGATTCAGCA 4739

Db 3622 CTGGCAGATCAAGGAGGAGGAAAAAATCTTAGGGCTCAACAGGAGAGTGGGATCAGCA 3681  
 QY 4740 GAACCAAGGCCAATATATGCTCCCTCTGCCACCGCAGCAGCACCACAAATCCAGCATCC 4799  
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 QY 4800 TTACATGCTCTCTCATCAGGCATCTCTTCTCAACATGGGGTAAACAAAATTTACTAA 4859  
 Db 3742 TTACATGCTCTCTCATCAGGCATCTCTTCTCAACATGGGGTAAACAAAATTTACTAA 3801  
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 Db 3802 TCAGTCTTAATTTAAAGCACATATGTTATGCAAGCTAGTTACGTTAGGTGTTCTGAATTTTC 3861  
 QY 4920 ATTGAAGTTATAGCTGTTAGTGATGTTATCATGATGCTAGATTTTGAAACTAGAAAATTT 4979  
 Db 3862 ATTGAAGTTATAGCTGTTAGTGATGTTATCATGATGCTAGATTTTGAAACTAGAAAATTT 3921  
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 Db 3922 TATTTTAAACATATATTTTATTAACGTAGGTTAATGCAATGGTGCACCAAGCAAACT 3981  
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 Db 4042 TGTGTGCTATGTTTAAAGTACAATTTTAAAGTACAATTTTAAAGTACAATTTTAAAGTACA 4101  
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 QY 5220 TACATATGCACTTTTCATATATATCTATGATGATTTGGAATGCAATGCTGATCAAG 5279  
 Db 4162 TACATATGCACTTTTCATATATATCTATGATGATTTGGAATGCAATGCTGATCAAG 4221  
 QY 5280 AGATGATCCAAATGGCAATGAGGAGGAATGATCTGAACTGATCTTGAAACCGTTTACA 5339  
 Db 4222 AGATGATCCAAATGGCAATGAGGAGGAATGATCTGAACTGATCTTGAAACCGTTTACA 4281  
 QY 5340 ACTGCAACCTTGGCTGCTGCGCGCATGA 5368  
 Db 4282 ACTGCAACCTTGGCCG-TTGGCGCGCATGA 4309

RESULT 3  
 ID AAC61415  
 XX AAC61415 standard; DNA; 4379 BP.  
 AC AAC61415;  
 XX  
 DT 19-FEB-2001 (first entry)  
 XX  
 XX Genomic DNA sequence encoding an APETALAI (API) polypeptide.  
 DE  
 XX APETALAI; API; floral meristem identity gene; CAULIFLOWER; CAL; LEAFY;  
 KW LFY; floral meristem; early flowering; ds.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FN US6127123-A.  
 XX  
 PD 03-OCT-2000.  
 XX  
 PE 09-SEP-1998; 98US-00149976.  
 XX  
 PR 26-JAN-1996; 96US-00592214.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Yanofsky MF;

XX MPI; 2000-618379/59.  
 DR Identifying a Brassica having a cauliflower phenotype involves detecting  
 PT a polymorphism associated with cauliflower locus comprising a modified  
 PT cauliflower allele that does not encode active cauliflower gene product.  
 XX Disclosure; Fig 10A-F; 93pp; English.  
 XX The present sequence represents the genomic sequence of an APETALAI (API)  
 CC gene. The API polypeptide is an ectopically expressible floral meristem  
 CC identity gene product. The specification also describes CAULIFLOWER (CAL)  
 CC and LEAFY (LFY) gene products. CAL is involved in the conversion of shoot  
 CC meristem to floral meristem. CAL is highly conserved among different  
 CC angiosperms. The CAL polynucleotides may be used to shoot meristem to  
 CC floral meristem, and to promote early flowering in angiosperms  
 XX Sequence 4379 BP; 1488 A; 706 C; 714 G; 1467 T; 0 U; 4 Other;  
 SQ  
 Query Match 58.8%; Score 3148.2; DB 3; Length 4379;  
 Best Local Similarity 80.1%; Pred. No. 0;  
 Matches 4301; Conservative 0; Mismatches 7; Indels 1061; Gaps 9;  
 QY 1 GAATCCCGGATCTCCATATACATATACATATATATATATATATATATATATATATATAT 60  
 Db 1 GAATCCCGGATCTCCATATACATATACATATATATATATATATATATATATATATATAT 60  
 QY 61 ATTCTCTATACACTATCTTTTAACTTATGATCGTTTCAAACTCAGGACGTCATGTT 120  
 Db 61 ATTCTCTATACACTATCTTTTAACTTATGATCGTTTCAAACTCAGGACGTCATGTT 120  
 QY 121 TTAATTTGGTATATAACACGACCATTTCAAGTATATATATATATATATATATATATATAT 180  
 Db 121 TTAATTTGGTATATAACACGACCATTTCAAGTATATATATATATATATATATATATATAT 180  
 QY 181 AATATAACTTCTATGAAGAAAATACATAAAGTTGGATTAAATGCAAGTGACATCTTTT 240  
 Db 181 AATATAACTTCTATGAAGAAAATACATAAAGTTGGATTAAATGCAAGTGACATCTTTT 240  
 QY 241 AGCATAGGTTTCATTTGGCATAGAAGAAATATATACTAAAAATGAACTTTAACTTAAATA 300  
 Db 241 AGCATAGGTTTCATTTGGCATAGAAGAAATATATACTAAAAATGAACTTTAACTTAAATA 300  
 QY 301 GATTTTACTATATACAAATTTTCTTTTACATGCTCTAAATTTATTTTCTTAAATTTAG 360  
 Db 301 GATTTTACTATATACAA-TTTTTCTTTTACATGCTCTAAATTTATTTTCTTAAATTTAG 359  
 QY 361 TATGATTTGTTTGTGATGAACAATAATACCGTAAGCAATAGTCTTAAAGATGTCCA 420  
 Db 360 TATGATTTGTTTGTGATGAACAATAATACCGTAAGCAATAGTCTTAAAGATGTCCA 419  
 QY 421 AATATTTATAAATTAACAAAGTAAATCAATAAGGAAGAGACACGTTGGAACACCAAAAT 480  
 Db 420 AATATTTATAAATTAACAAAGTAAATCAATAAGGAAGAGACACGTTGGAACACCAAAAT 479  
 QY 481 AAGAGAGAAATGGAAGAAAACAGAAAGAAATTTTAAACAGAAATCAATTTAGTCTCTC 540  
 Db 480 AAGAGAGAAATGGAAGAAAACAGAAAGAAATTTTAAACAGAAATCAATTTAGTCTCTC 539  
 QY 541 AAACCTGAGATATTTAAAGTAACTAACTAAACAGGAACACCTTGACTAAACAAAGAAATTT 600  
 Db 540 AAACCTGAGATATTTAAAGTAACTAACTAAACAGGAACACCTTGACTAAACAAAGAAATTT 599  
 QY 601 GAAATGTTGTCACATTTTCACTTAATATATATATTTTCTTAAAGGCTTATGCAATATATG 660  
 Db 600 GAAATGTTGTCACATTTTCACTTAATATATATTTTCTTAAAGGCTTATGCAATATATG 659  
 QY 661 CCTTAAGCAAAATGCCGAATCTGTTTTTTTTTTTGTATTTGATATTTGACTGAAATATAG 720  
 Db 660 CCTTAAGCAAAATGCCGAATCTGTTTTTTTTTTTGTATTTGATATTTGACTGAAATATAG 719  
 QY 721 GGGTTTTTTCACACTTGAAGATCTCAAAAGAGAAAATATTAACGCGAAATTCATTTGTA 780











QY 1081 TCGATCTTCTCTCTCTTCTTAAATCCTGCGTACAAATCCGTCGACGCAATACATTACAC 1140  
Db |||||  
QY 1078 TCGATCTTCTCTCTCTTCTTAAATCCTGCGTACAAATCCGTCGACGCAATACATTACAC 1137  
Db |||||  
QY 1141 AGTTGTCAATTTGGTCTCAGCTCTACCAAAAACATCTATTGCCAAAAGAAAGGCTCTATTT 1200  
Db |||||  
QY 1138 AGTTGTCAATTTGGTCTCAGCTCTACCAAAAACATCTATTGCCAAAAGAAAGGCTCTATTT 1197  
QY 1201 GTACTTCACCTGTTACAGCTGAGACATTAATAATAAAGCAAAATTTGATAAAAAGG 1260  
Db |||||  
QY 1198 GTACTTCACCTGTTACAGCTGAGACATTAATAATAAAGCAAAATTTGATAAAAAGG 1257  
QY 1261 GTTCTCACCTTATTCCAAAAGATAGTGTAAATAGGGTAATAGAGAAATGTTAATAAAA 1320  
Db |||||  
QY 1258 GTTCTCACCTTATTCCAAAAGATAGTGTAAATAGGGTAATAGAGAAATGTTAATAAAA 1317  
QY 1321 GGAATTAATAATAGATATTTGGTT - GGTTTCAGATTTTGTTCGTAGATCTACAGGAA 1379  
Db |||||  
QY 1318 GGAATTAATAATAGATATTTGGTTGGTTTCAGATTTGTTTCGTAGATCTACAGGAA 1377  
QY 1380 ATCTCGCGCTCAATGCAAAAGAGGTGACACTTGGGGAAGGACCGAGTGTCCGTACAA 1439  
Db |||||  
QY 1378 ATCTCGCGCTCAATGCAAAAGAGGTGACACTTGGGGAAGGACCGAGTGT - CGTACAA 1436  
QY 1440 TGTACTTACCATTTCTCTTCACGAGACGTCGATAATCAAAATGTTTATTTTCATATTT 1499  
Db |||||  
QY 1437 TGTACTTACCATTTCTCTTCAGAGACGTCGATAATCAAAATGTTTATTTTCATATTT 1496  
QY 1500 TTAAGTCGCGAGTTTATTAATAAATCATGGACCCGACATTTAGTACGAGATATACCAATG 1559  
Db |||||  
QY 1497 TTAAGTCGCGAGTTTATTAATAAATCATGGACCCGACATTTAGTACGAGATATACCAATG 1556  
QY 1560 AGAAGTCGACGCAATCTCTAAAGAAACCACTGTGGTTTTCGAAACAAGAGAAACGAG 1619  
Db |||||  
QY 1557 AGAAGTCGACGCAATCTCTAAAGAAACCACTGTGGTTTTCGAAACAAGAGAAACGAG 1616  
QY 1620 CTTTGTCTTTCCCTAAACCACTCTTACCAAAATCTCCATAAATAAGATCCCGAGA 1679  
Db |||||  
QY 1617 CTTTGTCTTTCCCTAAACCACTCTTACCAAAATCTCCATAAATAAGATCCCGAGA 1676  
QY 1680 CTCAAAACACAAGTCTTTTATAAGGAAAGAAAGAAACCTTCTCTAAATGGTTTCATACC 1739  
Db |||||  
QY 1677 CTCAAAACACAAGTCTTTTATAAGGAAAGAAAGAAACCTTCTCTAAATGGTTTCATACC 1736  
QY 1740 AAAGTCTGAGCTCTTCTTTATATCTCTCTGTAGTCTTCTTATGGGGTCTTTGTTTGT 1799  
Db |||||  
QY 1737 AAAGTCTGAGCTCTTCTTTATATCTCTCTGTAGTCTTCTTATGGGGTCTTTGTTTGT 1796  
QY 1800 TTGTTCTTTTAGAGTAAGAGTTTCTTAAAGAGGATCAAAATGGAGGGGTAGGGT 1859  
Db |||||  
QY 1797 TTGTTCTTTTAGAGTAAGAGTTTCTTAAAGAGGATCAAAATGGAGGGGTAGGGT 1856  
QY 1860 TCAATTGAAGAGGTAGAGAACCAAGATCAATAGACAAGTGCATTTCTCGAAAGAGAGC 1919  
Db |||||  
QY 1857 TCAATTGAAGAGGTAGAGAACCAAGATCAATAGACAAGTGCATTTCTCGAAAGAGAGC 1916  
QY 1920 TGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTGATGCTGAAAGTGTCTTGT 1979  
Db |||||  
QY 1917 TGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTGATGCTGAAAGTGTCTTGT 1976  
QY 1980 TGTCTTCTCCATAAGGGGAACTCTTTCGAATCTCCACGATTTCTGGTAACTTCACT 2039  
Db |||||  
QY 1977 TGTCTTCTCCATAAGGGGAACTCTTTCGAATCTCCACGATTTCTGGTAACTTCACT 2036  
QY 2040 AATTCCTTACTTTTAAAAAATCTTTTAACTGCTACTTTATATAGTTTTTTTCCCTT 2099  
Db |||||  
QY 2037 AATTCCTTACTTTTAAAAAATCTTTTAACTGCTACTTTATATAGTTTTTTTCCCTT - 2094  
QY 2100 AAGTGTACTTGTGATTTGCCTTAATTTATCACTACTGCTTTTGTATATATTTCTAGG 2159  
Db |||||  
QY 2095 - - - - - 2094  
QY 2160 GCTTCCATTTTGGATTTTGTATTAGCCAGAAAAATGTTTATACAAATTTGTATAATT 2219

Db 2095 - - - - - 2094  
QY 2220 TAAAAATCAAAACCTTTAGGCGCGTAGTGAAGTGAACCTAGAACACACAGATTATACCAT 2279  
Db 2095 - - - - - 2094  
QY 2280 AGTAATTTACCTTTGATATATTGTGCAATATTATCAGCATCANATCTTCAAACTCAAGAGA 2339  
Db 2095 - - - - - 2094  
QY 2340 TATAGAAGGATGCTTAATCTTTGAACTAGGTTTTCATCCCTAACTCAATGAACTCT 2399  
Db 2095 - - - - - 2094  
QY 2400 TTTGTTCTCCAATAGCCATGCTTTTCGAATTTGCAGATCTAAGCTCTAATTTGATGCCATA 2459  
Db 2095 - - - - - 2094  
QY 2460 GTAAGAAAAATAAGATCTGTAGTTTTCACCTCGCTCACTGAGTTCGAGTTTAAATGAAGTG 2519  
Db 2095 - - - - - 2094  
QY 2520 TCGTTTCTTTTTCATATATAGTTGCAACTGGAATTATAATTAATAAATAATTTATCGGACGA 2579  
Db 2095 - - - - - 2094  
QY 2580 GAAAAATAATTTAAAAATAGATATAGATAACAATGTCAAAATTGAGAAATTTTATTAGAAAG 2639  
Db 2095 - - - - - 2094  
QY 2640 AATATTAACTTAGAGTGTGTTTTTTTTCAGCTGTAAAGAAATATCTAAATTTGTTCTCAC 2699  
Db 2095 - - - - - 2094  
QY 2700 GACTGTCTTTCATGTTTTCGAATCTAAGCAAGAAATGTTTAAACTCGGATCTTAAG 2759  
Db 2095 - - - - - 2094  
QY 2760 ATTATGAACCTGTAATATAAACAACATATATAGTATTAAATTTGAACTAGTGTCTTCTT 2819  
Db 2095 - - - - - 2094  
QY 2820 TTGCTACTTTGACTTTAGAAATTTAAACTGAAACAAAGATGTCAAACTCTGAGTAGGAGT 2879  
Db 2095 - - - - - 2094  
QY 2880 CTTTGACCTCTGGGATCCATAAAGAACTAACTCCATCCTAAATCGGCTTCTTACC 2939  
Db 2095 - - - - - 2094  
QY 2940 ATGGTCAAACTTAGCTCCAAAGCAACAGCTGTCTTCTTTTTTTTTTTTTTTTTTTTT 2999  
Db 2095 - - - - - 2094  
QY 3000 TTTTAAGCATTTGCTTGTCTGAAAAAATAAGATTGGTTGATAAATTGGCAAGATTATAAT 3059  
Db 2095 - - - - - 2094  
QY 3060 AATTTATTATAATGTGTGCACTAAGAGATTTTCTGTACTAATTTGTAGCAAAATTTAA 3119  
Db 2095 - - - - - 2094  
QY 3120 GAAACCGCATTTAGAACTGAAGCTAAGCATAGGCTCTATGATTCATACTGTTTGT 3179  
Db |||||  
QY 2095 - - - - - -GGTCTATGATTCATACTGTTTGT 2119  
QY 3180 ATTATAAGGTATCATAGAGATCGGTACTTGTATTGTATAGGAAATCTTGGTTTAAATG 3239  
Db |||||  
QY 2120 ATTATAAGGTATCATAGAGATCGGTACTTGTATTGTATAGGAAATCTTGGTTTAAATG 2179  
QY 3240 CATAAACCATCATTAAGATTATCTTAAATGTGATGATTTTGGTCACATCTCCATAT 3299  
Db |||||





Db 1378 TCTCGCGTCAATCAAGCAAGTGACACTTGGGAGACAGTGGTCCGTACAT 1437  
 QY 1441 GTTACTTACCAATTTCTCTTACGAGAGTGCATTAATCAAAATGTTTATTTTATTTT 1500  
 Db 1438 GTTACTTACCAATTTCTCTTACGAGAGTGCATTAATCAAAATGTTTATTTTATTTT 1497  
 QY 1501 TAAAGTCGCGAGTTTATTAATAAATAATCATGACCCGACATTTAGTACGAGATATACCAATGA 1560  
 Db 1498 TAAAGTCGCGAGTTTATTAATAAATAATCATGACCCGACATTTAGTACGAGATATACCAATGA 1557  
 QY 1561 TAAAGTCGAGCAACCAATCTTAAGAAACCACTGTGTGTTTTTGCAGAAAGAGAAACCCAGC 1620  
 Db 1558 TAAAGTCGAGCAACCAATCTTAAGAAACCACTGTGTGTTTTTGCAGAAAGAGAAACCCAGC 1617  
 QY 1621 TTTAGTCTTTTCCCTAAACCACTTTTACCAATCTCTCCATAAATAAAGATCCGAGAC 1680  
 Db 1618 TTTAGTCTTTTCCCTAAACCACTTTTACCAATCTCTCCATAAATAAAGATCCGAGAC 1677  
 QY 1681 TCAAAACACAGTCTTTTATAAAGGAAGAAAGAAAGAAAGAAAGTCTTAAATGGTTTCATACCA 1740  
 Db 1678 TCAAAACACAGTCTTTTATAAAGGAAGAAAGAAAGAAAGAAAGTCTTAAATGGTTTCATACCA 1737  
 QY 1741 AAGTCTGAGCTCTCTTTATATCTCTCTTTGTAGTTTCTTTATGGGGTCTTTGTTTGT 1800  
 Db 1738 AAGTCTGAGCTCTCTTTATATCTCTCTTTGTAGTTTCTTTATGGGGTCTTTGTTTGT 1797  
 QY 1801 TGGTCTTTTATAGTAAGAGTTTCTTAAAGAGATCAA 1840  
 Db 1798 TGGTCTTTTATAGTAAGAGTTTCTTAAAGAGATCAA 1837

RESULT 6

AAV58319  
 ID AAV58319 standard; DNA; 1865 BP.  
 XX AC AAV58319;  
 XX DT 19-NOV-1998 (first entry)  
 XX XX Brassica oleracea API gene.  
 DE CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;  
 KW early flowering promotion; angiosperm; API gene; ds.  
 XX OS Brassica oleracea.  
 XX PN US811536-A.  
 XX PD 22-SEP-1998.  
 XX PF 26-JAN-1996; 96US-00592214.  
 XX PR 26-JAN-1996; 96US-00592214.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Yanofsky ME;  
 XX DR WPI; 1998-530945/45.  
 XX XX Cloned CAULIFLOWER genes - and vectors for converting shoot meristems to  
 PT floral meristems.  
 XX PS Disclosure; Fig 11; 93pp; English.  
 XX CC This sequence encodes the Brassica oleracea API protein. This sequence  
 CC was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER  
 CC (CAL) protein of the invention. An expression vector containing the CAL  
 CC DNA sequence can be used to convert shoot meristems to floral meristems,  
 CC especially to promote early flowering in angiosperms  
 XX SQ Sequence 1865 BP; 610 A; 315 C; 339 G; 596 T; 0 U; 5 Other;

Query Match 8.8%; Score 474.4; DB 2; Length 1865;  
 Best Local Similarity 60.1%; Pred No. 8.5e-71;  
 Matches 1199; Conservative 0; Mismatches 596; Indels 200; Gaps 17;  
 QY 3423 GCACCTGAGTCGAGCTCAATGATATTTCAATAAATATTTCTCTCTTTTAAATCCACATATAT 3482  
 Db 1 GCACCTGAGTCGAGCTCAATGATATTTCTCTCTCTTTTAAATCCACATATATATATAT 60  
 QY 3483 ATTATATCAATCTATTTTGTAGTATTTGATGAATTTTATTTGTATATAAACTTCTGGTACACA 3542  
 Db 61 ATTATTTTCAGTATTTAGTATATATA-----CTTATCTGTATTTAACTTTGTAGATATA 113  
 QY 3543 GACAACTGGTCGATGGAGTATAACAGGCTTAAGGCTTAAGCTTAAGCTTTTGGAGAGAAA 3602  
 Db 114 GACGAACCTGGTCGATGGAGTATATAGGCTTAAGGCTTAAGCTTTTGGAGAGAAA 173  
 QY 3603 CCAGAGGTACACATTT--TACACTCATCATTTTCTATCTAGAAAATCGATCGGGTCCAT 3660  
 Db 174 CCAGAGGTACATTTTTCATTCATTTATATATAGATGAATATCAACAGGATTAAT 233  
 QY 3661 -----TTTAAAGTAAGTTTAAATTT 3679  
 Db 234 GTTAGTTTAAATATGATGATTTACTTTATAGAAAATGATGATTTTAAATACAAAATAATG 293  
 QY 3680 CATTCATG--CTATTGAAATTCAGGCATTTCTTGGGGAAGACTTGCAGAGCAATGAGCC 3737  
 Db 294 CATCATGCTCTATTGAAATTTAGGCATTTCTTGGGGAAGACTTGCAGAGCAATGAGCC 353  
 QY 3738 TAAAGAGCTTCAAGATCTGGAGCAGCTTGCACACTGCTCTTAAAGCAGCATCGGACTAG 3797  
 Db 354 TAAAGGAACCTCCAGAACTTAGAGCAACAGCTTGATCTGCTCTTAAAGCAGCATCGGCTTAG 413  
 QY 3798 AAAAGTATTCCTCTCTGCTATTTCTTGAACATATCTATATTAACCTTAAAGCTTTACAAGT 3857  
 Db 414 AAAAGTATGAATCCTCTCTATTTCTTTAAATTAACATGTATACAACTTAAAC----- 463  
 QY 3858 GTTATTATAATGTGAACATTTGAATACATATGTGTATGTATCAATATATATATATATATAT 3917  
 Db 464 -----ACATATTTTATTATTTCAATACATATATATATATATATATATATATATAT 508  
 QY 3918 CAATATCAATTTGATATGCTATAGTGGTTGCGATGTATAGTATATGTTGTATTTT 3977  
 Db 509 GTGATTTTATGTTGGATATATAAAGATCAATCAGCTCGATTTAGATGT--ATGACTTTTTA 567  
 QY 3978 AAGACTCCATATTTACTTAAAGTAATGGGTTGTTTAAATGTTGATGTGTGTATGCGAAGCC 4037  
 Db 568 AAGAAATTAGTATATAGATATGATTAGTCAATGTAAATGTTGATGTGTGTATGCGAAGCC 627  
 QY 4038 AACTTTATGTACGAGTCCATCAATGAGCTCCAAAAAAGGTATGTAAAAACCCCTATCAAAAT 4097  
 Db 628 AACTTTATGTACGAGTCCATCAATGAGCTCCAAAAAAGGTATGTAAAAACCCCTATCAAAAT 687  
 QY 4098 GTATGTCTTTATAGAGAAACGTATAGAAA-----GCTAATTAACAATCGTGGCG 4146  
 Db 688 TGACGTTTACATAGAAATTAACGCTGTAAGAAATCCTATAGGGGAGCTAAACAATCGTGGCG 747  
 QY 4147 TTTTCGGAATGACAGGAGAGGCCATACAGGAGCAAAACAGCATGCTTTCTTAAACAGGTA 4206  
 Db 748 TTTTCGGAATGACAGGAGAGGCCATACAGGAGCAAAACAGCATGCTTTCTTAAACAGGTA 807  
 QY 4207 ACACATGTATCATTTCTTTTCAATCAACATGTTGTCCATTTGCATTTACTTGTACCTTCCA 4266  
 Db 808 CCATTTGTATTTTATATATCGTCAAAATGTTTCTTATTGTAGTACTTTAGCTTCCA 867  
 QY 4267 CTGTTCTGTCTCACACTTCCAGCAGCTATACCTACGATATCTTCAATCTCCACTTAA 4326  
 Db 868 CTGTTCTACTCCACACTTCCAGCAGCTATACCTACCTACGATATCTTCCACAGGATTTCCACA 927  
 QY 4327 CTTTCGSCACCATTAATAAATAAAGAAATCTTTGCAAAATTTGTTTGAATATAGCATAGAT 4386  
 Db 928 TATTTCTCCACTTAGCTTCGGCACCACCTATAACT--AAAATATAGATAAATAATATATTTT 986









CC encodes a floral meristem identity gene product (see AAW23812) that is involved in the conversion of shoot meristem to floral meristem. Mutation of the *API* gene results in replacement of a few basal flowers by inflorescence shoots that are not subtended by flowers. When *API* is ecotypically expressed in shoot meristem, the shoot meristem is converted to floral meristem and early flowering can occur. The invention relates to floral meristem identity genes *API*, *LFY* and especially *CAL* (see AAT76885-97 and AAT99437) and their use in converting shoot meristem to floral meristem and in promoting early flowering in transgenic plants, especially angiosperms such as cereal plants, leguminous plants, oilseed plants, trees, fruit-bearing plants or ornamental flowers

xx  
SQ Sequence 1860 BP; 610 A; 315 C; 339 G; 596 T; 0 U; 0 Other;

Query Match 8.8%; Score 470.4; DB 2; Length 1860;  
Best Local Similarity 60.8%; Pred. No. 4e-70;  
Matches 1213; Conservative 0; Mismatches 576; Indels 207; Gaps 19;

QY 3423 GCACCTGAGTCCGAGTCAATGTATTTCAATAAATATTTCTCTTTTAAATCCACATATAT 3482  
DB 1 GCACCTGAGTCCGAGTCCCAATGTAACCAATTTCTCTCCATTAATATATAAATTAAT 60

QY 3483 ATTATATCAATATTTGTAGTATTTGATGAATTTTATTGTATAAAACTTCTGTACACA 3542  
DB 61 ATTATTTCAATTTAGTGATATA-----CTTATCTGTATTAACCTTTGTGATATA 113

QY 3543 GACAACTGTCGATGAGTATTAACAGGCTTAAGGCTTAAGCTTAAGCTTTTGAGAGAAA 3602  
DB 114 GAGCACTGTCGATGAGTATTAATAGCTTAAGGCTTAAGCTTTTGAGAGAAA 173

QY 3603 CCAGAGTACACATT--TACACTCATCACATTTCTATCTAGAAATCGATCGGTTCCAT 3660  
DB 174 CCAGAGTACATTTTCATTCATCTTATTAATAGATGAATATCAAAACAGATTAAT 233

QY 3661 -----TTTAAAGTAAGTTAAAT 3679  
DB 234 GTTAGTTAAAAATGCATGATTACTTATAAGAAATGATGATTAATAACAAAATG 293

QY 3680 CATTGATG--CTATGAAATTCAGGONTATCTTTGGGAAAGACTTGAAGCAATAGAGCCC 3737  
DB 294 CATCGATGCTCTATTTGAAATTTAGGCACTATCTTTGGGAAAGACTTGAAGCAATAGAGCCC 353

QY 3738 TAAAGAGTCTCAGATCTCGAGAGAGCTTGACACTGCTTTAAGCACATCCGCACTAG 3797  
DB 354 TAAGAACTCCAGAACTTAGAGCAACAGCTTGATGATCTCTTAAGCACATCCGCTCTAG 413

QY 3798 AAAAGTATTCCTCTCTCTATTTCTGTTGAACATATCTATATAACTTAAACGTTTACAAGT 3857  
DB 414 AAAAGTATGAATCCTCTCTATTTCTTTAATTAACATGTATACAACCTTAAAC----- 463

QY 3858 GTTATTATATGTGAACATTTGAATACATATGTATGTATGATCAATATATATCAGTAAT 3917  
DB 464 -----ACATATTTATTTTATTTCAATATACATATATATGATGATGATATAT 508

QY 3918 CAATATCAATTTTGATATGCTATAGTGTGCTTGAATGTATGATGATGATGATGATTTT 3977  
DB 509 GTGATTTTATGTTGGATATAAAGATCAATCAGCTCGATGATGATGATGATGATGAT 567

QY 3978 AAGACTCCATTTACTTAAAGTAAATGGTTGTTTAAATGTTGATGTTGATGATGATGATGAT 4037  
DB 568 AAGAAATTTAGTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627

QY 4038 AACTTATGACGAGTCCATCAATGAGCTCCAAAAGAGGTATGTAACCCCTATCAAAAT 4097  
DB 628 AACTTATGACGAGTCCATCAATGAGCTCCAAAAGAGGTATGTAACCCCTATCAAAAT 687

QY 4098 GTATGCTTATAGAGAACTGATAGGAA-----GCTAATTTAAACAATCGTCCG 4146  
DB 688 TGACGTTTACATAGATTAATCTGCTGTGAATATCTTATAGGGAGCTTAACAATCGTCCG 747

QY 4147 TTTTCGAAATGACAGAGAAAGGCCATACAGGAGCAAAACAGCATGCTTTCTAAACAGGTA 4206  
DB 748 TTTTCGAAATGACAGAGAAAGGCCATACAGGAGCAAAACAGCATGCTTTCTAAACAGGTA 807

QY 4207 ACACATGTCATCAATTTCTCTTTTCATCAACAAATGTTGTCATGTCATTTACTGTTACCTTCCA 4266  
DB 808 CCATTTGTCATTTATTTTATATCGTCAAAATGTTTCTTATTTAGTACTGTTAGCTTTCCA 867

QY 4267 CTCTTCGTCACACCTTCCAGCCAGACTATACCTAGATATCTTCATATCTCCACTTAA 4326  
DB 868 CTGTTCTACTCCACACTTTCAAGCCAGACTATACCTACTAGACTAGAGATTTCTCCACA 927

QY 4327 CTTTCGACCACTTAAATAAATAAGAAATCTTTGCAAAATTTGTTGAAATAGCATAGAT 4386  
DB 928 TATTTCTCCACTTTAGCTTCGGCACCACTATACT-AAAAATAGATAAATAATCAITTTT 986

QY 4387 GTTGTCTATTGATGATATAAATCACAGCCTGTACGTAGATATG- GTTGTCTCGTTTGTAGT 4445  
DB 987 ATAGTCTA-TGATGATATATCTGTCAGCCAGTACGTAGTTGGGTATTTGCCGTTTGTAGT 1045

QY 4446 TTTAAGG-TGTCCTCTCGGATTGAAATATTTTGAATCTTTTGAATGTTTGTGCCCCATCA 4504  
DB 1046 TTTAAGGTTCTTTTCCGGAATTGAAATATTTTACCTTACCTTTGATGCTATTATATGATATA 1105

QY 4505 TTCTTACTTACTGCTCATATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4564  
DB 1106 TCTATTTAGAGTCTGCTTTGAAATTTGATGATGATA---TGTATGTTATGATGTTGG 1161

QY 4565 TATAATAGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4624  
DB 1162 TAACAAACTGTTGTTGAAATTTGAAAT----- 1189

QY 4625 TATAGTTTCTTCACTTTGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4684  
DB 1190 -----TGTC 1193

QY 4685 AGATCAAGGAGAGGAAAAAATTTCTTAGGCTCAACAGGAGCAGTGGGATCAGCAGAAACC 4744  
DB 1194 AGATTAAGGAGAGGAAAAAGTTCTTAGGCGCAACAGAGCAATGGGAGCAGCAGAAACC 1253

QY 4745 AAGCCACAAATATGCTTCCCTCTGTCACCGCAGCAGCAACCAATCCAGATCTCTTACA 4804  
DB 1254 ATGGCCA-TATATGCTCTCGCTCCACCCCGCAGCAGCATCAATCCAGATCTCTTACA 1312

QY 4805 TGCTCTCTCATCAGCATCTCTCTTTCTCAACATGGGTAAACAAAAATTTACTTAATCAGT 4864  
DB 1313 TGCTCTCTCATCAGCATCTCTCTTTCTCAACATGGGTAAACAAAAATTTACTTAATCAGT 1372

QY 4865 CTTTAAATTAAGCACATATGTTTATGCAAGCTAGTTAGTGTGTTGTTGTTGTTGTTGTTGTT 4924  
DB 1373 ---ACTTTCAAGTCATATGTTATATATACAGATAGTTAGTGTATTAAGTCCAGTGA 1428

QY 4925 AGTTATAGCTGTTAGTGTGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4984  
DB 1429 GTTAGGTTGTTGTTAGTGTGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1488

QY 4985 TAAACAT-TATTTTATTAACGTTAGTTAATGCAATGGTCCCAACGCAACAACTTAT 5043  
DB 1489 TCAGTTATATAATTAAGTATGATCATCATCAATCAATGCTGTTAAACAGACTTATA 1548

QY 5044 AGTGTGGAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5103  
DB 1549 TTTTTCGAAA--GTAGATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1606

QY 5104 GGTCTATG-----TGTTTAAAGTACAAATTTTGTAGTATGATGATGATGATGATGATGATGATGAT 5159  
DB 1607 CGTATTTATTTGTTTCAAAATTAACCTTGAGGTAGTTAGTAAATAAATATATCTTTGATA 1666

QY 5160 TTGACATTTTCAACATGCTGATATTTGATTTTCTCTTCTGTTGACGTTGAAACATATGAT 5219  
DB 1667 TGCCCTTTTACCAATTTTCACTACAAACATGTTGATATTTTTCAGCAAC-----TATG 1716

QY 5220 TACATATGCACTTTTCAATATATATATATATATATATATATATATATATATATATATATATATAT 5279  
DB 1717 TAGATAATTTGTAAGCTATATCATGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1776

QY 5280 AAGATGATCCCAATGCAATGAGGAGGAATGATCTCGAACTGACTCTTGAACCCGTTTACA 5339  
 DB 1777 AAGAAGATCAATGCAATGAGGAGGAACGATCTCGATCTGTCTTGAACCCGTTTACA 1836  
 QY 5340 ACTGCAACCTTGGCTG 5355  
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RESULT 9  
 AAV58320  
 ID AAV58320 standard; DNA; 2185 BP.  
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 AC AAV58320;  
 XX  
 DT 19-NOV-1998 (first entry)  
 XX  
 DE Brassica oleracea API gene.  
 XX  
 KW CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;  
 KW early flowering promotion; angiosperm; API gene; ds.  
 XX  
 OS Brassica oleracea.  
 XX  
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 XX  
 PD 22-SEP-1998.  
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 PF 26-JAN-1996; 96US-00592214.  
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 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Yanofsky MF;  
 XX  
 DR WPI; 1998-530945/45.  
 XX  
 PT Cloned CAULIFLOWER genes - and vectors for converting shoot meristems to  
 PT floral meristems.  
 PS Disclosure; Fig 12; 93pp; English.  
 XX  
 CC This sequence encodes the Brassica oleracea API protein. This sequence  
 CC was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER  
 CC (CAL) protein of the invention. An expression vector containing the CAL  
 CC DNA sequence can be used to convert shoot meristems to floral meristems,  
 CC especially to promote early flowering in angiosperms  
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 SQ Sequence 2185 BP; 719 A; 353 C; 409 G; 698 T; 0 U; 6 Other;

Query Match 7.3%; Score 390.4; DB 2; Length 2185;  
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 QY 3358 TGTATGATGAGAGATGATCTTGAACCGTATGAGAGGTACTCTTACGCCGGAAGACAGC 3417  
 DB 413 TGAACAGTATGAGGAGATGATCTTGAACCGTATGAGAGGTACTCTTACGCCGGAAGACAGC 472  
 QY 3418 TTATTTGACCTGAGTCCGAGCGTCAATGATTTTCAATAAATATTTCTCCCTTTAAATCCACA 3477  
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 QY 3478 TATATATATATCAATCTATTTGTAGTATGATGAATTTTATTTGATATAAACTTCTGCT 3537  
 DB 533 TAAATATATTTTCAATCTATTTGTAGTATGATGAATTTTATTTGATATAAACTTCTGCT 585  
 QY 3538 ACACAGACAACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3597

DB 586 ATATAGACCAAATCTGTCGATGGAGTATAATAGGCTTAAGGCTTAAGATGAGCTTTTGGAG 645  
 QY 3598 AGAAACCAAGAGGTACACATTTTACATCTACATCTTCTATCTAGAAA-ATCGATCGGTTT 3656  
 DB 646 AGAAACCAAGAGGTACATTTTTCATTCATTTATATATATGATGAAATATCAACAGGAT 705  
 QY 3657 CCAT-----TTTAAAGTAAGTTAA 3675  
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 QY 3676 AATTCATTTGATG--CTATTGAAATTCAGGCAATTTCTTTGGGGAAGACATTTGCAAGCAATGA 3733  
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 QY 3854 AAGTGTATATATATGAGCAATTTGAATAATATATGATGATGATGATGATGATGATGATGAT 3913  
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 QY 4263 TCCACTGTTCTGCTCCACACTTCCAGCAAGCTATACCTACGATATCTTCATATCTCCAC 4322  
 DB 1339 TCCACTGTTCT--CACCACACTTCAAGCCAGCTATACCTAC----- 1378  
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 DB 1379 -----CTACGACTAC 1388  
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OY 5319 TGACTCTTGAACCGCTTACAACTGCAACCTTGGCTG 5355
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RESULT 12
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AC AAC37677;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18266.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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QY 1871 GGATAGAGAACAGATCAATAGACAGTGCATCTCTCGAAAGAAAGAGCTGGTCTTTTGA 1930
Db 181 GGATAGAGAACAGATCAATAGACAGTGCATCTCTCGAAAGAAAGAGCTGGTCTTTTGA 240

QY 1931 AGAAGCTCATGATCTCTGTTCTCTGTCATGCTGAGTGTCTTGTGTTGTTCTCTCCC 1990
Db 241 AGAAGCTCATGATCTCTGTTCTCTGTCATGCTGAGTGTCTTGTGTTGTTCTCTCCC 300

QY 1991 ATAAGGGAAACTCTTCGAATCTCCACTGATTTCTTG 2027
Db 301 ATAAGGGAAACTCTTCGAATCTCCACTGATTTCTTG 337

RESULT 14
AA15016
ID AA15016 standard; cDNA; 1220 BP.
AC AA15016;
XX
XX
XX 21-AUG-2000 (first entry)
DE cDNA encoding the Arabidopsis API protein.
KW API; promoter; transgenic plant; suppressed flowering; wood;
KW agamous-like protein; floral organ selective regulatory element; ss.
XX
XX Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 141..911
FT /*tag= a
FT /product= "API protein"
XX
XX WO200023578-A2.
XX
XX 27-APR-2000.
XX
XX 15-OCT-1999; 99WO-US024407.
XX
XX 16-OCT-1998; 98US-0104604P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Yanofsky MF;
XX
XX WPI; 2000-339680/29.
XX
```

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DR P-PSDB; AAY84912.
XX
XX Transgenic plants in which flowering is suppressed by a tissue specific
XX cytotoxic gene product, useful for the production of wood for use as
XX lumber or pulp.
XX
XX Disclosure; Fig 8a-b; 79pp; English.
XX
XX The present sequence encodes the Arabidopsis API protein. The API
XX promoter is used to produce transgenic plants of the invention, which are
XX characterized by suppressed flowering. The plants are transformed with a
XX construct comprising a floral organ selective regulatory element (e.g.
XX API promoter), operatively linked to a nucleotide sequence encoding a
XX cytotoxic gene product (which is inheritable by the progeny). The plants
XX may be grown for either human consumption or for use as a raw material in
XX industry. When trees, they are particularly suitable for cultivation in
XX typical wood. As the flowering process consumes 20-35% of the energy of a
XX typical plant, it is advantageous to suppress flowering in order to
XX improve wood and lumber yields. Suppression of flowering may be desired
XX to eliminate the production of allergic pollen, or to prevent pollen
XX dissemination
XX
XX Sequence 1220 BP; 405 A; 235 C; 249 G; 331 T; 0 U; 0 Other;
XX
XX Query Match 5.8%; Score 311.4; DB 3; Length 1220;
XX Best Local Similarity 99.7%; Pred. No. 2.6e-43; Indels 0; Gaps 0;
XX Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1715 AAAACCTTTCCTAATGGTTTCATACCAAGTCTGAGCTCTTCTTTATATCTCTCTGTAGT 1774
Db 13 AGAACCTTTCCTAATGGTTTCATACCAAGTCTGAGCTCTTCTTTATATCTCTCTGTAGT 72

QY 1775 TCTTATTTGGGGTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAAG 1834
Db 73 TCTTATTTGGGGTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAAG 132

QY 1835 GATCAAAATGGGAAGGGTAGGGTTCATTTGAAGAGGATAGAGACCAAGTCAATAGAC 1894
Db 133 GATCAAAATGGGAAGGGTAGGGTTCATTTGAAGAGGATAGAGACCAAGTCAATAGAC 192

QY 1895 AAGTGACATTCTCGAAAAAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTT 1954
Db 193 AAGTGACATTCTCGAAAAAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTT 252

QY 1955 TCTGTGATGCTGAAGTTGCTTTGTTGTTGTTCTTCCCATAGGGGAACTCTTGAATACT 2014
Db 253 TCTGTGATGCTGAAGTTGCTTTGTTGTTGTTCTTCCCATAGGGGAACTCTTGAATACT 312

QY 2015 CCACTGATTTCTTG 2027
Db 313 CCACTGATTTCTTG 325

RESULT 15
AA186628
ID AA186628 standard; DNA; 1057 BP.
XX
XX AC AA186628;
XX
XX 18-JUN-1998 (first entry)
XX
XX APETAL1 gene from Arabidopsis thaliana.
XX
XX Transgenic plant; ectopically expressed; meristem gene; APETAL1; API;
XX CAULIFLOWER; CAL; LEAFY; LFY; reproductive development; angiosperm; ds.
XX
XX Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX CDS 124..894
XX /*tag= a
XX /product= "API gene_product"
XX
XX
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 18:14:38 ; Search time 19962 Seconds  
(without alignments)  
11655.416 Million cell updates/sec

Title: US-09-869-582-12  
Perfect score: 5368  
Sequence: 1 gaattccggatctccata.....ttggctgcttcgcgcgatga 5368

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl :

- 1: gb\_ba.\*
- 2: gb\_btg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	5100.4	95.0	99698	8	AC008262	AC008262 Genomic s
2	4486.2	83.6	4708	8	AF466783	AF466783 Arabidops
3	4464.4	83.2	4710	8	AF466778	AF466778 Arabidops
4	4462.4	83.1	4711	8	AF466779	AF466779 Arabidops
5	4457	83.0	4710	8	AF466776	AF466776 Arabidops
6	4457	83.0	4711	8	AF466782	AF466782 Arabidops
7	4451	82.9	4712	8	AF466777	AF466777 Arabidops
8	4449.2	82.9	4709	8	AF466773	AF466773 Arabidops
9	4445	82.8	4710	8	AF466784	AF466784 Arabidops
10	4444.2	82.8	4711	8	AF466780	AF466780 Arabidops
11	4441.4	82.7	4709	8	AF466771	AF466771 Arabidops
12	4440	82.7	4707	8	AF466772	AF466772 Arabidops
13	4429.2	82.5	4705	8	AF466781	AF466781 Arabidops
14	4427	82.5	4706	8	AF466785	AF466785 Arabidops
15	4414.2	82.2	4709	8	AF466775	AF466775 Arabidops
16	4412.2	82.2	4706	8	AF466774	AF466774 Arabidops
17	3148.2	58.6	4379	6	AR042847	AR042847 Sequence
18	3148.2	58.6	4379	6	AR111355	AR111355 Sequence
19	2858.8	53.3	4847	8	AF466786	AF466786 Arabidops
20	2020.6	37.6	3638	8	AF143379	AF143379 Arabidops
21	1790.4	33.4	1838	6	AX411721	AX411721 Sequence
22	1142	21.3	1177	6	AX411722	AX411722 Sequence
23	474.4	8.8	1865	6	AR042848	AR042848 Sequence
24	474.4	8.8	1865	6	AR111356	AR111356 Sequence
25	415.4	7.7	1786	8	AF126726	AF126726 Brassica
26	414.4	7.7	1786	8	AF126734	AF126734 Brassica
27	410.2	7.6	1786	8	AF126725	AF126725 Brassica
28	408.4	7.6	1785	8	AF126723	AF126723 Brassica
29	404.2	7.5	1781	8	AF126724	AF126724 Brassica
30	390.4	7.3	2185	6	AR042849	AR042849 Sequence
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32	387.6	7.2	411	8	ATH522563	AJ522563 Arabidops
33	339	6.3	1165	8	AY087956	AY087956 Arabidops
34	325.4	6.1	1172	8	BT004113	BT004113 Arabidops
35	324.4	6.0	1537	8	AF126727	AF126727 Brassica
36	310.2	5.8	1782	8	AF126730	AF126730 Brassica
37	309	5.8	1778	8	AF126728	AF126728 Brassica
38	303.8	5.7	1054	6	AR063254	AR063254 Sequence
39	303.8	5.7	1054	6	ATAP1	Z16421 A.thaliana
40	303.8	5.7	1057	6	AR095090	AR095090 Sequence
41	303.8	5.7	1057	6	AR200414	AR200414 Sequence
42	293.4	5.5	1785	8	AF126733	AF126733 Brassica
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44	288.6	5.4	1786	8	AF126732	AF126732 Brassica
45	288.6	5.4	1787	8	AF126722	AF126722 Brassica

ALIGNMENTS

RESULT 1  
AC008262/c  
LOCUS AC008262  
DEFINITION Genomic sequence for Arabidopsis thaliana BAC F4N2 from chromosome 1, complete sequence.  
ACCESSION AC008262  
VERSION AC008262.4 GI:5757471  
KEYWORDS HTG.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 99698)  
AUTHORS Shinn, P., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Khan, S., Kim, C.,

[illegible]



Qy	1502	AAGTCCGACGTTTTATTAAAAAATCATGGACCGGACATTAGTACGAGATATACCAATGAG	1561
Db	38298	AAGTCCGACGTTTTATTAAAAAATCATGGACCGGACATTAGTACGAGATATACCAATGAG	38239
Qy	1562	AAGTCGACACGCAAAATCTTAAGAAACCACTGTGTGTTTTTGCAAACAAGAGAAACGACT	1621
Db	38238	AAGTCGACACGCAAAATCTTAAGAAACCACTGTGTGTTTTTGCAAACAAGAGAAACGACT	38179
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Db	38178	TTAGCTTTTCCCTAAACCACTCTTACCMAATCTCTCCATAAATAAAGATCCCGAGACT	38119
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Qy	1742	AGTCTGAGCTCTTCTTTATAATCTCTTGTGTAGTTCTTATATGGGGGTCTTTGTTTGTGTTT	1801
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Qy	1922	GTCCTTTTGAAGAAAGCTCATAGATCTCTGTTCTCTGTGATGCTGAAGTTGCTCTTGTTG	1981
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Qy	1982	TCTTCTCCCATAAAGGGGAAACTCTTCGAATACCTCCATCATTTCTTGGTAACCTTCAACTAA	2041
Db	37818	TCTTCTCCCATAAAGGGGAAACTCTTCGAATACCTCCATCATTTCTTGGTAACCTTCAACTAA	37759
Qy	2042	TTCTTTTACTTTTTAAAAAATCTTTTAACTGCTACTTTATATATAGTTTTTTCCTCCCTTAA	2101
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Qy	2102	GTTGACTACTTGATTTGCCCTAAATTAATCACTACTGCTTTTG - TTATATATTTTCTAGGG	2160
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Qy	2161	CTTCCATTTTTCGATTTTTTTGATTAGCCAGAAAAATGTTTAACAAAATTTGTTATAATTT	2220
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Db	37519	GTAATTTACCTTGATATATTGTGCAATATTATCAGCATCATATCTTCAAACTCAAGAGCA	37460
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Db	37459	TATAGAAGGGGTATGTTTAACTTTGAACTAGGGTTTTGATCCCTAACTCATAAATGAAT	37400
Qy	2397	CTTTTTTGTCTCCAATAGCCATGCTTTTCGAATTTTCAGATCTAAGCTCTAAATGTGATGCC	2456
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Qy	2457	ATAGTAAGAAAATAAGATCTGATGTTTTTCACTCGCTCACTGAGTTTCGAGTTTTTAAATGAA	2516
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37039	Db		TAAGATTATGAACCTCGTAATATAAAACACATATATAGTATTAATTTGAACTAGTGTGCT	36980
2816	Qy		TCCTTTGCTACTTTGACTTTTGAATTTAAACCTGAAACCAAGATGTCAAATCTGAGTAGG	2875
36979	Db		TCCTTTTCTA-TTTGACTTTTGAATTTAAACCTGAAACCAAGATGTCAAATCTGAGTAGG	36921
2876	Qy		GAGTCTTTGACCTCTCGGGATCCATAAAAGAACTAACTCCATCTCAAAATCGGCTTCTT	2935
36920	Db		GAGTCTTTGACCTCTCGGGATCCATAAAAGAACTAACTCCATCTCAAAATCGGCTTCTT	36861
2936	Qy		ACCGATGGTCAAACTTTAGCTCCAAACGAACAGCAGCTGTTCTCTTTTTTTTTTTTTTT	2995
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2996	Qy		TTTTTTTTTAAGCAATCTGCTGTTCTGAAAAAAATAAGATGGTAAATTTGGCAAGATTA	3055
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3175	Qy		TTGTTATTTATAAAGGTATCATAGAGATCGGTACTTGATTTGTTATAGGAAATCTTGGTTT	3234
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3295	Qy		CATATTTATTTATATAATAAATCATATTTGGTTGATGATAAAGCTAACCTCAATTTCTGTG	3354
36500	Db		CATATTTATTTATATAATAAATCATATTTGGTTGATGATAAAGCTAACCTCAATTTCTGTG	36441
3355	Qy		AAATGATCAGTATGGAGAAGATCTTGAACGCTATGAGAGGTACTCTTACGCCGGAAGAC	3414
36440	Db		AAATGATCAGTATGGAGAAGATCTTGAACGCTATGAGAGGTACTCTTACGCCGGAAGAC	36388
3415	Qy		AGCTTATTTGCACCTGAGTCCGACGTCAATGTTTTCATATAATTTTCTCTTTTAAATCC	3474
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3475	Qy		ACATATATTTATATCAATCTATTTGTAGTATTCATGAATTTTTTATTTGATATAAACTTCT	3534
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3535	Qy		GGTACACAGAAACCTGGTCGATGGAGTATAACAGGCTTAAGCTTAAGATTGAGCTTTTG	3594
36260	Db		GGTACACAGAAACCTGGTCGATGGAGTATAACAGGCTTAAGCTTAAGATTGAGCTTTTG	36201
3595	Qy		GAGGAAACACAGAGGTACATTTTACACTCATACATTTCTATCTAGAAATTCGATCGGG	3654
36200	Db		GAGGAAACACAGAGGTACATTTTACACTCATACATTTCTATCTAGGAAATCGATCGGG	36141
3655	Qy		TTCCATTTTAAAGTAAGTTAAATTCATGTCATTTGAATTCAGGCAATTCATTGGG	3714

Db 36140 TTCCATTTTAAAGTAAGTTAAATTCATTGATGCTATTGAAATTCAGGCATTATCTTGGG 36081  
QY 3715 GAAGACTTGAAGCAATGAGCCCTTAAGAGCTTCAGAACTTGGAGCAGCAGCTTGACACT 3774  
Db 36080 GAAGACTTGAAGCAATGAGCCCTTAAGAGCTTCAGAACTTGGAGCAGCAGCTTGACACT 36021  
QY 3775 GCTCTTAAGCACATCCGACCTAGAAAAAGTATTGCTCTCTGCTATTTCGTTGAAACATATCT 3834  
Db 36020 GCTCTTAAGCACATCCGACCTAGAAAAAGTATTGCTCTCTGCTATTTCGTTGAAACATATCT 35961  
QY 3835 ATATACTTAAACGTTTACAGTGTATTATAATATGTAACCAATTTGAAATACATATGCTAT 3894  
Db 35960 ATATACTTAAACGTTTACAGTGTATTATAATATGTAACCAATTTGAAATACATATGCTAT 35901  
QY 3895 GTATCAATATATATATCAGTAATCAATATCAATTTGATATGCTATATAGTTGGTTGCAAT 3954  
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QY 3955 GTATGAGTTATGTTGCTATTATTAAGACTCCATATTAATTAAGCTAATGGTTGTTAATG 4014  
Db 35840 GTATGAGTTATGTTGCTATTATTAAGACT - CATATTACTTAAGTAATGGTTGTTAATG 35782  
QY 4015 TTGATGCTGTATGACAGAACCAACTTATGACAGTCCATCAATCAGCTCCAAAAAAA 4074  
Db 35781 TTGATGCTGTATGACAGAACCAACTTATGACAGTCCATCAATCAGCTCCAAAAAAA 35722  
QY 4075 GGTATGTAACCCCTATCAAAATGATGTCTTATAGAGAAACGATATAGGAAAGCTAATTA 4134  
Db 35721 GGTATGTAACCCCTATCAAAATGATGTCTTATAGAGAAACGATATAGGAAAGCTAATTA 35662  
QY 4135 ACAATCGTGGCTTTCGGAAATGACAGAGAGGCCATAGAGGAGCAAAACAGCATGCTT 4194  
Db 35661 ACAATCGTGGCTTTCGGAAATGACAGAGAGGCCATAGAGGAGCAAAACAGCATGCTT 35602  
QY 4195 TCTAAACAGGTAACACATGTATCATCTTCTTTTCATCAACATGTTGCTCCATTGCAATAC 4254  
Db 35601 TCTAAACAGGTAACACATGTATCATCTTCTTTTCATCAACATGTTGCTCCATTGCAATAC 35542  
QY 4255 TGTATCCTTCCACTGTTCTGCTCCAGCTTCCAGCAGCTATACCTACGATATCTTCAT 4314  
Db 35541 TGTATCCTTCCACTGTTCTGCTCCAGCTTCCAGCAGCTATACCTACGATATCTTCAT 35482  
QY 4315 ATCTCCACTTAACTTCGGCACCATTAAATAAATAAGAAATCTTTCGAAATGTTTGA 4374  
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QY 4435 GTCCGTTTAGTTTAAAGG-TGTCCTCGGATTGAAATATTTTGAATCTTTTGAATG 4493  
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QY 4613 CCATTGCATATATAGTTTCTTCACTTTGAAAATGATGATGATATATATGTTTGAAT 4672  
Db 35187 CCATTGCATATATATAGTTTCTTCACTTTGAAAATGATGATGATATATATGTTTGAAT 35128  
QY 4673 AAAATTTGCTCGCAGATCAAGGAGGGAATAATCTTAGGGCTCCAGCAGCAGTGGG 4732  
Db 35127 AAAATTTGCTCGCAGATCAAGGAGGGAATAATCTTAGGGCTCCAGCAGCAGTGGG 35068  
QY 4733 ATCAGCAGAACCAAGGCCACAAATATGCTCCCTCTGCCCACCGCAGCAGCAGCAATCC 4792  
Db 35067 ATCAGCAGAACCAAGGCCACAAATATGCTCCCTCTGCCCACCGCAGCAGCAGCAATCC 35008

QY 4793 AGCATCCTTACATGCTCTCTCATCAGCCATCTCCTTTCTCAACATGGGGTAACAAAAA 4852  
Db 35007 AGCATCCTTACATGCTCTCTCATCAGCCATCTCCTTTCTCAACATGGGGTAACAAAAA 34948  
QY 4853 TTACTAATCAGTCTTAAATTTAAAGCACATATGTTATGCAAGCTAGTTACGTTAGGTGTTG 4912  
Db 34947 TTACTAATCAGTCTTAAATTTAAAGCACATATGTTATGCAAGCTAGTTACGTTAGGTGTTG 34888  
QY 4913 TAATTTCAITGAACTTAGCTGTTAGTGATGGTTTACATGATG-CTAGATTTTGAACATA 4971  
Db 34887 TAATTTCAITGAACTTAGCTGTTAGTGATGGTTTACATGATGATGATGATGTTTGAACATA 34828  
QY 4972 GAAAACTTTATTTTAAACATTAATTTTAAACCTAGGTTAAATGCAATGGTTCGCAAAACG 5031  
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DEFINITION Arabidopsis thaliana Ler apetala 1 (AP1) gene, partial cds.  
ACCESSION AP466783  
VERSION AP466783.1 GI:20799363  
KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 4708)  
Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and  
Purugganan,M.D.  
Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral  
Developmental Pathway  
Genetics 160 (4), 1641-1650 (2002)  
21969421  
11973317

JOURNAL MEDLINE  
PUBMED  
REFERENCE 2 (bases 1 to 4708)  
AUTHORS Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and  
Purugganan,M.D.  
Direct Submission  
Submitted (09-JAN-2002) Genetics, North Carolina State University,  
Campus Box 7614, Raleigh, NC 27695-7614, USA  
Location/Qualifiers

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QY	4235	CATGTTGTCATGCAATCTGTTTACCTTCCACTGTTCTGCTCCACACTTCCAGCAAGC	4294	QY	5311	TCCTGAACTGACTCTTTGAAACCCGTTTACAACTGCAACCTT 5350	
Db	3598	CATGTTGTCATGCAATCTGTTTACCTTCCACTGTTCTGCTCCACACTTCCAGCAAGC	3657	Db	4671	TCCTGAACTGACTCTTTGAAACCCGTTTACAACTGCAACCTT 4710	
QY	4295	TATACCTAGCATATCTTCATATCTTCACTTAACTTCGGACCATTAATAAATAATAGAAA	4354				
Db	3658	TATACCTAGCATATCTTCATATCTTCACTTAACTTCGGACCATTAATAAATAATAGAAA	3717				
QY	4355	ATCTTTGCAAAATTTGTTGAAATAGCATAGATGTTGTTTATGTTGATGATATATACCCAG	4414				
Db	3718	ATCTTTGCAAA-TTGTTTGAATAGCATAGATGTTGTTTATGTTGTTGTTGTTGTTGTTG	3776				
QY	4415	CTGTAGCTAGATATGTTTGTGCGTTTATGTTTAAAGG-TGTCTCTCGATTGAAATAT	4473				
Db	3777	CTGTAGCTAGATATGTTTGTGCGTTTATGTTTAAAGG-TGTCTCTCGATTGAAATAT	3836				

## RESULT 4

AP466779	4711 bp	DNA	linear	PLN 15-MAY-2002
LOCUS	Arabidopsis thaliana Kas-1 apetal 1 (AP1) gene, partial cds.			
DEFINITION	Arabidopsis thaliana			
ACCESSION	AP466779			
VERSION	AP466779.1	GI:20799355		
KEYWORDS	Arabidopsis thaliana (thale cress)			
SOURCE	Arabidopsis thaliana			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			

REFERENCE	1 (bases 1 to 4711)
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purugganan,M.D.
TITLE	Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral Developmental Pathway
JOURNAL	Genetics 160 (4), 1641-1650 (2002)
MEDLINE	21969421
PUBMED	11973317
REFERENCE	2 (bases 1 to 4711)
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purugganan,M.D.
TITLE	Direct Submission
JOURNAL	Submitted (09-JAN-2002) Genetics, North Carolina State University, Campus Box 7614, Raleigh, NC 27695-7614, USA
FEATURES	Location/Qualifiers source 1..4711 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="903" /ecotype="Kas-1" <1203..>4711 /gene="API1" /note="APETA1A1" join(<1203..1387,2730..2808,2909..2973,3067..3166,3398..3439,3526..3567,4047..4201,4627..>4711) /gene="API1" /product="apetala 1" join(1203..1387,2730..2808,2909..2973,3067..3166,3398..3439,3526..3567,4047..4201,4627..>4711) /gene="API1" /codon_start=1 /product="apetala 1" /protein_id="AA28455.1" /db_xref="GI:20799356" /translation="MGGRVQLKRIENKINQVTFKRRAGLLKKAHEISVLCDAEVFA LVFSGKLUFEVSDCMCKILERYRYAERQLIAPESDVNTWMSYNRKAKAI ELLERNRSHYLGEDLQMSKELQQLDALKHTRKQNLMYESINELQKKEKA IQFQNSMLSKQIKEREKILRAQOEQWQDQNGHMPPLPPQHQIQHPYMLSHQSPSP FLNNGGLYQEDDPAMRRNDLELTLEPVYCNL"
gene	
mRNA	
CDS	
ORIGIN	
Query Match	83.1%; Score 4462.4; DB 8; Length 4711;
Best Local Similarity	98.9%; Pred. No. 0;
Matches 4671; Conservative	0; Mismatches 27; Indels 23; Gaps 17;
QY	643 AGGCTTATGCAATATATGCGCTTAAGCAAAATGCCGAATCTG--TTTCTTTTCTTTTGTATT 700
Db	1 AGGCTTATGCAATATATGCGCTTAAGCAAAATGCCGAATCTGTTTTTTTTTTTTTTTGTATT 60
QY	701 GGATATTGACTGAAAAATAAGGGGTTTTTTCACACTTGAAGATCTCAAAAGAGAAAACCTAT 760
Db	61 GGATATTGACTGAAAATAAGGGGTTTTTTCACACTTGAAGATCTCAAAAGANAAAACCTAT 120
QY	761 TACAACGGAAATTCATTGTTAAAAGAGTGATTAAAGCAAAATTGACAAAGGTTTTTATGTG 820
Db	121 TACAACGGAAATTCATTGTTAAAAGAGTGATTAAAGCAAAATGACAAAGGTTTTTATGTG 180
QY	821 GTTTATTTCATTATATGATTGCATCAAAATCTATATATGTTGTTTATTATTACAAT 880
Db	181 GTTTATTTCATTATATGATTGCATCAAAATCTATATATGTTGTTGTTTATTATTACAAT 240
QY	881 ATATATGGATATAACGTFACAAACTAAATATGTTGTTGATGAGAAAAAAAATATATGTATG 940
Db	241 ATATATGGATATAACGTFACAACTAAATATGTTGATGAGAAAAAAAATATGTATG 300
QY	941 TTTGATTACCAATAGCACATATTCAACTGATTTTGTCTCTGATCATCTACAACTTAAT 1000
Db	301 TTTGATTACCAATAGCACATATTCAACTGATTTTGTCTCTGATCATCTACAACTTAAT 360
QY	1001 AAGAAACACACAACTTGAAAAAATCTTTGCAAAAATACATATTTTGGGTTGAAATTTTG 1060
Db	361 AAGAAACACACAACTTGAAACAACTTTTGCAAAAATACATATTTTGGGTTGAAATTTTG 420

Qy	2141	TTG-TTATATATTTTCTAGGCGTTCCATTTTGGATTTTTCGATTTAGCCAGAAAAATGTT	2199
Db	1500	TTGTTTATATATTTTCTAGGCGTTCCATTTTGGATTTTTCGATTTAGCCAGAAAAATGTT	1559
Qy	2200	TAATACAAATTTCTATAATTTAAAAATCAAACTTTAGGGCCGTAGTGAAGTGAACCCCTA	2259
Db	1560	TAATACAAATTTCTATAATTTAAAAATCAAACTTTAGGGCCGTAGTGAAGTGAACCCCTA	1619
Qy	2260	GAACACACAGATTTATACCATAGTAATTTACCTTCATATATTGTCATATTTTATCAGCATC	2319
Db	1620	GAACACACTAATTTATACCATAGTAATTTACCTTCATATATTGTCATATTTTATCAGCATC	1679
Qy	2320	ATATCTTCAAACTCAAGAG-ATATAGAAGGGTAT--GTTAAATCTTTTGAACTAGGGTTTT	2375
Db	1680	ATATCTTCAAACTCAAGAGCATATAGAAAGGTGTATGTTTAACTTTTGAACTAGGGTTTT	1739
Qy	2376	GATCCCTAACTCATATGAATGAAATCCTTTTGTCTCCAAATAGCCATGCTCTTTCGAAATTTGCGAG	2435
Db	1740	GATCCCTAACTCATATGAATTTCTTTTGTCTCCAAATAGCCATGCTCTTTCGAAATTTGCGAG	1799
Qy	2436	ATCTAAGCTCTAATTTGATGTCATAGTAAGAAATAAGATCTGTAGTTTTCACCTCGCTCAC	2495
Db	1800	ATCTAAGCTCTAATTTGATGTCATAGTAAGAAATAAGATCTGTAGTTTTCACCTCGCTCAC	1859
Qy	2496	TGAGTTCGAGTTTTAAATGAAGTGTCTGTTTCTTTTTCATATAT-AGTTGCAACTCGAAT	2554
Db	1860	TGAGTTCGAGTTTTAATTTGAAGTGTCTGTTTCTTTTTCATATATAGTTTGCACCTCGAAT	1919
Qy	2555	ATAATTAATAAATAATTAATGGAACGAGAAAAATAATTTAAATAGATATAGATACAATGTC	2614
Db	1920	ATAATTAATAAATAATTAATGGAACGAGAAAAATAATTTAAATAGATATAGATACAATGTC	1979
Qy	2615	AAATTTGAGAAATTTTATTAAGAAGATATTTAACTTACGAGTGTGTTTTTTTTCAGCTGT	2674
Db	1980	AAATTTGAGAAATTTTATTAAGAAGATATTTAACTTACGAGTGTGTTTTTTTTCAGCTGT	2039
Qy	2675	AAAAGAATATCTAATTTGTTCTCACGACTGTGCTCTCATGTTTTGCAATCTAAGCAAAG	2734
Db	2040	AAAAGAATATCTAATTTGTTCTCACGACTGTGCTCTCATGTTTTGCAATCTAAGCAAAG	2099
Qy	2735	AAAAATGTTTAAACTCGGAATCTTAAGATATGAACCTCGTAAATATAAAACACTATAGTAT	2794
Db	2100	AAAAATGTTTAAACTCGGAATCTTAAGATATGAACCTCGTAAATATAAAACACTATAGTAT	2159
Qy	2795	TAAATTTGAATAGTGTGCTCTTTTTCGCTACTTTTGACTTTAGAAATTAAGAACTGAACA	2854
Db	2160	TAAATTTGAATAGTGTGCTCTTTTTCGCTACTTTTGACTTTAGAAATTAAGAACTGAACA	2218
Qy	2855	AAGATGTCAAATCTGAGTAGGGAGTCTTTTGACCTCTGGGATCCATAAAAAGAACTAACT	2914
Db	2219	AAGATGTCAAATCTGAGTAGGGAGTCTTTTGACCTCTGGGATCCATAAAAAGAACTAACT	2278
Qy	2915	CCATCCTAAATCGGCTCTTACCGATGGTCAAACTTAGCTTCCAAAGCAAGCTGTT	2974
Db	2279	CCATCCTAAATCGGCTCTTACCGATGGTCAAACTTAGCTTCCAAAGCAAGCTGTT	2338
Qy	2975	CTTCTTTTTTTTTTTTTTTTTTTTTTTTTTAAGCATGTCCTGTGTTCTGAAAAAAAATAAG	3034
Db	2339	CTTCTTTTTTTTTTTTTTTTTTTTTTTTTTAAGCATGTCCTGTGTTCTGAAAAAAAATAAG	2398
Qy	3035	ATTGTTAAATTTGGCAAGATTATAATAATTTATTAATGTCGCA-CTAAGAAGATTTTT	3093
Db	2399	ATTGTTAAATTTGGCAAGATTATAATAATTTATTAATGTCGCACTAAGAAGATTTTT	2458
Qy	3094	CTGTACCTTAATTTGTAGCAAAATTAAGAAACCGGAGTTTAGAACTCGAGCTAAGAGCAT	3153
Db	2459	CTGTACCTTAATTTGTAGCAAAATTAAGAAACCGGAGTTTAGAACTCGAGCTAAGAGCAT	2518
Qy	3154	GGGTCTATGATTCATCTGTTTTTGTATTATTAAGGATATCATAGAGTCGGTACTGATT	3213
Db	2519	GGGTCTATGATTCATCTGTTTTTGTATTATTAAGGATATCATAGAGTCGGTACTGATT	2578
Qy	3214	TGTTATAGAAATCTTTGGTTTAATTTGCAATAAAACCATCATTTAGATTTTATCATAAATGTC	3273









QY	3095	TGTACCTAATTGTAGCAAAATTAAGAGAAACCGCAGTTAGTAACTCGAAGCTTAAGAGCATAG	3155
Db	2459	TGTACCTAATTGTAGCAAAATTAAGAGAAACCGCAGTTAGTAACTCGAAGCTTAAGAGCATAG	2518
QY	3155	GGTCTATGANTCATCTGTTTGGTTATTATATAAAGGTATCATAGAGATCGGTACTTGATTTT	3214
Db	2519	GGTCTATGANTCATCTGTTTGGTTATTATATAAAGGTATCATAGAGATCGGTACTTGATTT	2578
QY	3215	GTTATAGAAATCTTGGTTTAAATTCGCATATAAACCATCATTTAGATTTATCCTAAAATGTGA	3274
Db	2579	GTTATAGAAATCTTGGTTTAAATTCGCATATAAACCATCATTTAGATTTATCCTAAAATGTGA	2638
QY	3275	TCATATTTTGGTCACATCTCCATATTTATTATATAAATAAGTATAATTCGGTTCATGATA	3334
Db	2639	TGATATTTTGGTTACAATCTCCATATTTATTATATAAATAAGTATAATTCGGTTCATGATA	2698
QY	3335	AAGCTAACCCTAATCTGTGAAATGATCAGTATGGAGAAGATATCTTGAACGCTATGAGAG	3394
Db	2699	AAGCTAACCCTAATCTGTGAAATGATCAGTATGGAGAAGATATCTTGAACGCTATGAGAG	2758
QY	3395	GTACTCTTACGCCGAAGACAGCTTTATTCGACCTGAGTCCGACGCTCAATGTATTTCAATA	3454
Db	2759	GTACTCTTACGCCGAAGACAGCTTTATTCGACCTGAGTCCGACGCTCAATGTATTTCAATA	2818
QY	3455	AATATTTCTCCTTTTAAATCCACATATATATATATCAATCTATTTGTAGTATTGATGAAT	3514
Db	2819	AATATTTCTCCTTTTAAATCCACATATATATATCAATCTATTTGTAGTATTGATGAAT	2878
QY	3515	TTTTATTGTATAAAACHTCTGGTACACAGACAACCTGGTCGATGGAGTATAACAGGCTTA	3574
Db	2879	TTTTATTGTATAAAACHTCTGGTACACAGACAACCTGGTCGATGGAGTATAACAGGCTTA	2938
QY	3575	AGGCTAAGATTGAGCTTTTCGAGAGAAACACAGAGGTACATATTACACTCATCACATTTTC	3634
Db	2939	AGGCTAAGATTGAGCTTTTCGAGAGAAACACAGAGGTACATATTACACTCATCACATTTTC	2998
QY	3635	TATCTAGAAATCGATCGGGTTCATATTTTAAAGTAAAGTTAAAAATTCATTGATGCTATTGA	3694
Db	2999	TATCTAGAAATCGATCGGGTTCATATTTTAAAGTAAAGTTAAAAATTCATTGATGCTATTGA	3058
QY	3695	AATTCAAGCATATCTTTGGGGAAGACCTTGCAAGCAATGAGCCCTTAAAGACTTTCAGAATC	3754
Db	3059	AATTCAAGCATATCTTTGGGGAAGACCTTGCAAGCAATGAGCCCTTAAAGACTTTCAGAATC	3754
QY	3755	TGGAGCAGCAGCTTGACACTGCTTTAAGCACATCCGCACTAGAAAAGTATTGCCCTTCG	3814
Db	3119	TGGAGCAGCAGCTTGACACTGCTTTAAGCACATCCGCACTAGAAAAGTATTGCCCTTCG	3178
QY	3815	CTATTTCTGTTGAACATATCTATATAACTTAAACGGTTTACAAGTGTATTATTAATGTGAAC	3874
Db	3179	CTATTTCTGTTGAACATATCTATATAACTTAAACGGTTTACAAGTGTATTATTAATGTGAAC	3238
QY	3875	AATTGAATACATATGTATGTATCAATATATATATATCATGTAATCAATATTCATATTCAT	3934
Db	3239	AATTGAATACATATGTATGTATCAATATATATATATCATGTAATCAATATTCATATTCAT	3298
QY	3935	GTCTATAGGTTGGTTCGAATGTATGAGTTATGTTGTATTTTAAAGACCTCCATATTACATT	3994
Db	3299	GTCTATAGGTTGGTTCGAATGTATGAGTTATGTTGTATTTTAAAGACCTCCATATTACATT	3357
QY	3995	AAAGTAAATGGGTTGTTAAATGCTGTGTGTATGCAGAACCAACTTATGTACAGAGTCC	4054
Db	3358	AAAGTAAATGGGTTGTTAAATGCTGTGTGTATGCAGAACCAACTTATGTACAGAGTCC	3417
QY	4055	ATCAATGAGCTCCAAAAAAGGTATGTAAAAACCCCTATCAAAATGTATGTCTTATAGAAA	4114
Db	3418	ATCAATGAGCTCCAAAAAAGGTATGTAAAAACCCCTATCAAAATGTATGTCTTATAGAAA	3477
QY	4115	ACGTATAGGAAAGCTAATTAAACAATCGTCCGTTTCGGAAATACACAGGAGAGGCCATAC	4174
Db	3478	ACGTATAGGAAAGCTAATTAAACAATCGTCCGTTTCGGAAATACACAGGAGAGGCCATAC	3537

QY	4175	AGGAGCAAAACAGCAGTCTTTCTTAAACAGGTAACACATGTCTCATTTCTCTTTTCATCAA	4234
DB	3538	AGGAGCAAAACAGCATGCTTTCTAAACAGGTAAACACATGTCTCATTTCTCTTTTCATCAA	3597
QY	4235	CATGTTGTCATTCATTCATGTTTACCTTCCACATGTTCTGCTCCACACTTCCAGCCAGC	4294
DB	3598	CATGTTGTCATTCATTCATGTTTACCTTCCACTGTTCTGCTCCACACTTCCAGCCAGC	3657
QY	4295	TATACCTACGATATCTTTCATATCTCCACTTAACCTTCGGCACCATTAATAAATAAATAGAAA	4354
DB	3658	TATACCTACGATATCTTTCATATCTCCACTTAACCTTCGGCACCATTAATAAATAAATAGAAA	3717
QY	4355	ATCTTTGCAAAATTTGTTTGAATAAGCATPAGATGTGTCTATTTGATTCATATAATCACCAG	4414
DB	3718	ATCTTTGCAAA--TTGTTTGAATAAGCATAGATGTTGTCTATTGATTGATATAATCACCAG	3776
QY	4415	CCTGTACGTAGATATGGTTTGTTCGGTTAGTTTAAAGG--TGTCCTCGGATTGAAAATAT	4473
DB	3777	CCTGTACGTAGATATGGTTTGTTCGGTTAGTTTAAAGGTTGTCTCTCGGATTGAAAATAT	3836
QY	4474	TTTGAAATCTTTTGAATGTTTGTGCCCATCATTCCTTACTTTAGTCTCATCTATGCTATATG	4533
DB	3837	TTGAAA-----CTTTGAAATGTTGTGCCCATCTTC--TACTTAGTCTCATCTATGCTATATG	3891
QY	4534	AATATAGACACTACTCTCTAATAT--AAAAATTTAATAATAGTTCATTCATGAGTCAACT	4592
DB	3892	AATATAGACACTACTCTCTAATATTAATAAATAGTTTATAATAGTTCATTCATGAGTCAACT	3951
QY	4593	GTGAAAATAACTATTTCGTAAACATTGCATATATATAGTTTCTTCACATTCGAAAATTTGATG	4652
DB	3952	GTGAAAATAACTATTTCGTAAACATTGCATATATATAGTTTCTTCACATTCGAAAATTTGATG	4011
QY	4653	ATGATAATATGTTTGAATAAAATTTCTCGCAGATCAAGGAGAGGAAAAATTTCTTAG	4712
DB	4012	ATGATAATATGTTTGAATAAAATTTCTCGCAGATCAAGGAGAGGAAAAATTTCTTAG	4071
QY	4713	GGCTCAACAGAGCAGTGGGATCAGCAGAACCAAGGCCACAATATGCTCTCCCTCTGCC	4772
DB	4072	GGCTCAACAGGAGCAGTGGGATCAGCAGAACCAAGGCCACAATATGCTCTCCCTCTGCC	4131
QY	4773	ACCGCAGCAGCACCNAATCCAGCATCTTACATGCTCTCTCATCAGGCATCTCCTTTTCT	4832
DB	4132	ACCGCAGCAGCACCNAATCCAGCATCTTACATGCTCTCTCATCAGGCATCTCCTTTTCT	4191
QY	4833	CAACATGGGGTAAACAAAAATTAATAATCAGTCTTAATTTAAAGCACATATGTTATGCAA	4892
DB	4192	CAACATGGGGTAAACAAAAATTAATAATCAGTCTTAATTTAAAGCACATATGTTATGCAA	4251
QY	4893	GCTAGTTACGTTAGGTGTTGTAATTTCAATGAAAGTTATAGCTGTTAGTGATGTTTACATG	4952
DB	4252	GCTAGTTACGTTAGGTGTTGTAATTTCAATGAAAGTTATAGCTGTTAGTGATGTTTACATG	4311
QY	4953	ATG--CTAGATTTTCAACTAGAAAATCTTTATTTTAAAAATTTATTTTATTAACGTAGGTT	5011
DB	4312	ATGTCATGATTTTGAACATAGAAAATCTTTATTTTAAAAATTTATTTTATTAACGTAGGTT	4371
QY	5012	AATGCAATGTCGCCAAACGAAACAAATCTTATTAGTGTGAAAAATGTCATCATGGAATGGTT	5071
DB	4372	AATGCAATGTCGCCAAACGAAACAAATCTTATTAGTGTGG--AAATGTACATGAATGGTT	4430
QY	5072	GCAGAAAGCCTAAGTCGAC--TTTTGTGTTGTTGGTCTATGTTTAAAGTACAAATTTTAG	5130
DB	4431	GCAGAAAGCCTAAGTCGACCTTTTGTGTTGTTGGTCTATGTTTAAAGTACAAATTTTAG	4490
QY	5131	TTTGTGTAGATAAATGAAATTAATATATCTTTGACATTTTCACATGCACTGATATTTGATT	5190
DB	4491	TTTGTGTAGATAAATGAAATTAATATATCTTTGACATTTTCACAAATGGACTGATATTTGATT	4550
QY	5191	TTCTCTTGTGTTGACGGTGAACAATATGATATGCACTTTTCATATATATCTTATATCTATGTA	5250
DB	4551	TTCTCTTGTGTTGACGGTGAACAATATGATATGCACTTTTCATATATATCTTATATCTATGTA	4610
QY	5251	TGATTTGTAATCAGTGGTCTGTGTATCAAGAAGATATCCAATGGCAATGAGAGGAATGCA	5310

Db	4611	TGATGTGAATGCGAGTGTCTGTATCAAGAAGATGATCCTATGGCAATGAGGAGGATGA	4670	QY	761	TACACCGAAATTCATTTGTATAAAGCAAGTGATTAAGCAAAATTCAGCAAAAGGTTTTTATGTG	820
				Db	121	TACACCGAAATTCATTTGTATAAAGCAAGTGATTAAGCAAAATTCAGCAAAAGGTTTTTATGTG	180
QY	5311	TCTCGAATCTGCTCTTGAACCGGTTTCAACTGCAACCTT	5350	QY	821	GTTTATTTTCAATATGATTCACATCAAAATTTGTATATATATATGTTGTTTATTTAAACAAT	880
Db	4671	TCTCGAATCTGCTCTTGAACCGGTTTCAACTGCAACCTT	4710	Db	181	GTTTATTTTCAATATGATTCACATCAAAATTTGTATATATATATGTTGTTTATTTAAACAAT	240
RESULT 6				QY	881	ATATATGGATATAAGTACAAACTAAATATGTTGTTGATTGACGAAAAAATAATATATGATG	940
LOCUS	AF466782	4711 bp	DNA	linear	PLN 15-MAY-2002		
DEFINITION	Arabidopsis thaliana Col apetala 1 (AP1) gene, partial cds.			Db	241	ATATATGGATATAAGTACAAACTAAATATGTTGTTGATTGACGAAAAAATAATATATGATG	300
ACCESSION	AF466782			QY	941	TTTGATTAAACAATAGCACATATTTCAACTGATTTTGTCTCTGATCATCTACAACTTAAT	1000
VERSION	AF466782.1	GI:20799361		Db	301	TTTGATTAAACAATAGCACATATTTCAACTGATTTTGTCTCTGATCATCTACAACTTAAT	360
KEYWORDS				QY	1001	AAGAACAACAATTTGAAAAAATCTTTGACAAATATCTATTTTGGGTTTGAAATTTG	1060
SOURCE	Arabidopsis thaliana (thale cress)			Db	361	AAGAACAACAATTTGAAAAAATCTTTGACAAATATCTATTTTGGGTTTGAAATTTG	420
ORGANISM	Arabidopsis thaliana			QY	1061	AATCTTACAATTTATTTCTCTCGATCTTCTCTCTCTTCTTAAATCTCTGCGTACAAATCC	1120
REFERENCE	1 (bases 1 to 4711)			Db	421	AATCTTACAATTTATTTCTCTCGATCTTCTCTCTCTTCTTAAATCTCTGCGTACAAATCC	480
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purugganan,M.D.			QY	1121	GTGACGCAATACATACACAGTTGTCAATTTGGTCTCAGCTCTACCAAAACATCTATT	1180
TITLE	Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral Developmental Pathway			Db	481	GTGACGCAATACATACACAGTTGTCAATTTGGTCTCAGCTCTACCAAAACATCTATT	540
JOURNAL	Genetics 160 (4), 1641-1650 (2002)			QY	1181	GCCAAAAGAAAGTCTATTTGTTTCTACTTCTAGCTGTACAGCTGACAAATTAATATAAAG	1240
MEDLINE	21969421			Db	541	GCCAAAAGAAAGTCTATTTGTTTCTACTTCTAGCTGTACAGCTGACAAATTAATATAAAG	600
PUBMED	11973317			QY	1241	CAAAATTTGATAAACAAGGGTTCTCACCTTATTTCCAAAAGAAATAGTGTAAATAGGGTA	1300
REFERENCE	2 (bases 1 to 4711)			Db	601	CAAAATTTGATAAACAAGGGTTCTCACCTTATTTCCAAAAGAAATAGTGTAAATAGGGTA	660
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purugganan,M.D.			QY	1301	ATAGAGAATGTATAATAAAGAAATTAATAATAGATATTTTGGTGGTTCAGATTTGT	1360
TITLE	Direct Submission			Db	661	ATAGAGAATGTATAATAAAGAAATTAATAATAGATATTTTGGTGGTTCAGATTTGT	720
JOURNAL	Submitted (09-JAN-2002) Genetics, North Carolina State University, Campus Box 7614, Raleigh, NC 27695-7614, USA			QY	1361	TTCTGTAGATCTACAGGAAATCTCCGCGTCAATCAAGCAAGGAGTGCACCTTGGGAA	1420
FEATURES	Location/Qualifiers			Db	721	TTCTGTAGATCTACAGGAAATCTCCGCGTCAATCAAGCAAGGAGTGCACCTTGGGAA	780
Source	1. .4711			QY	1421	GGACCAAGTGGTCCGTACAATGTTACTTACCCATTTCTTTCACGAGACGTCGATAATCAA	1480
gene	/organism="Arabidopsis thaliana"			Db	781	GGACCAAGTGGTCCGTACAATGTTACTTACCCATTTCTTTCACGAGACGTCGATAATCAA	840
mRNA	/mol_type="genomic DNA"			QY	1481	ATTGTTTATTTTCATATTTTAAAGTCCGAGTTTATTAATAAATCATGACCCGACATTT	1540
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	/gene="AP1"			Db	901	AGTACGAGATATACCAATGAGAGTGCACACGCAATCTTAAAGAAACCACTGTGGTTT	960
	/note="APETALA1"			QY	1601	TGCAAAACAAGAGAAACCCAGCTTTAGCTTTTCCCTAAACCACTTTTACCCAAATCTCTCC	1660
	join(<1203..1387,2730..2808,2909..2973,3067..3166,3398..3439,3526..3567,4047..4201,4627..>4711)			Db	961	TGCAAAACAAGAGAAACCCAGCTTTAGCTTTTCCCTAAACCACTTTTACCCAAATCTCTCC	1020
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	join(1203..1387,2730..2808,2909..2973,3067..3166,3398..3439,3526..3567,4047..4201,4627..>4711)			Db	1021	ATAAATAAGATCCCGAGACTCAACACAGTCTTTTATAAGAGAAAGAAAGAAACT	1080
	/gene="AP1"			QY	1721	TTCTTAATTTGGTTTATACCAAGTCTGAGCTCTTCTTTTATCTCTCTTCTAGTCTCTTA	1780
	/codon_start=1			Db	1081	TTCTTAATTTGGTTTATACCAAGTCTGAGCTCTTCTTTTATCTCTCTTCTAGTCTCTTA	1140
	/product="apetala 1"			QY	1781	TTGGGGTCTCTTGTGTTTGTGTTTCTTTTAGAGTAAAGAGTTTCTTAAAAAGGATCAA	1840
	/protein_id="AA028458.1"			Db	1141	TTGGGGTCTCTTGTGTTTGTGTTTCTTTTAGAGTAAAGAGTTTCTTAAAAAGGATCAA	1200
	/db_xref="GI:20799362"			QY	1841	AAATGGGAAGGGGTAGGGTTCAATTGAGAGGATAGAGAACAGATCAATAGACAAGTGA	1900
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	LVVSHKGLFVSTDSCKEILERYSAEROLIAPESDVNTWMSYENRNLKAKI						
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ORIGIN							
Query Match	83.0%;	Score	4457;	DB	8;	Length	4711;
Best Local Similarity	98.9%;	Pred.	No. 0;				
Matches	4669;	Conservative	0;	Mismatches	30;	Indels	23;
				Gaps			17;
QY	643	AGGCTTATGCAATATATGCTTAAAGCAAAATGCCGAATCTG--TTTCTTTTCTTTTGTATT	700	Db	1	AGGCTTATGCAATATATGCTTAAAGCAAAATGCCGAATCTGTTTCTTTTCTTTTGTATT	60
QY	701	GGATATTGACTGAAATTAAGGGTTTTCACACTTGAAGATCTCAAAAGAGAAACTAT	760	Db	61	GGATATTGACTGAAATTAAGGGTTTTCACACTTGAAGATCTCAAAAGAGAAACTAT	120

Db	1201	 AAATGGGAAGGGTAGGGTTCAAATTGAGAGGATAGAGAAACAAGATCAATAGACAAGTGA	1260
Qy	1901	CATTCTCGAAAAGAAGAGCTGGTCTTTTTGAAGAAAGCTCATGAGATCTCTCTGTTCTCTGTG	1960
Db	1261	CATTCTCGAAAAGAAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTG	1320
Qy	1961	ATGCTGAAGTTGCTCTTGTTGTCCTCTCCCAATAAGGGGAAACTCTTGAATACTCCACTG	2020
Db	1321	ATGCTGAAGTTGCTCTTGTTGTCCTCTCCCAATAAGGGGAAACTCTTGAATACTCCACTG	1380
Qy	2021	ATTCCTTGCTAACTCAACTAAATCTTTACTTTTAAAAAAATCTTTTAATCTGCTACTTTTA	2080
Db	1381	ATTCCTTGCTAACTCAACTAAATCTTTACTTTTAAAAAAATCTTTTAATCTGCTACTTTTA	1440
Qy	2081	TATAGTTTTTTTTTCCCCCTTAAGTTGACTACTTGATTTTGCCCTAAATTTTCACTACTGCTT	2140
Db	1441	TATAG-TTTTTTCCCCCTTAAGTTGACTACTTGATTTTGCCCTAAATTTTCACTACTGCTT	1499
Qy	2141	TTG-TTATATATTTTCTAGGCTTCCATTTTTTGGATTTTTTGAATTTTTGATTAGCCAGAAAAATGTT	2199
Db	1500	TTGTTTATATATTTCTAGGCTTCCATTTTTTGGATTTTTTGAATTTTTGATTAGCCAGAAAAATGTT	1559
Qy	2200	TAATACAAATTTGTATATATTTAAAAATCAAAACTTTAGGGCGGTAGTGAAGTGAACCCCTA	2259
Db	1560	TAATACAAATTTGTATATATTTAAAAATCAAAACTTTAGGGCGGTAGTGAAGTGAACCCCTA	1619
Qy	2260	GAACACACAGATTATACCATAGTAATTACCTTGATATATTGTGCAATATTTATCAGCATC	2319
Db	1620	GAAACACTAATTATACCATAGTAATTACCTTGATATATTGTGCAATATTTATCAGCATC	1679
Qy	2320	ATATCTTCAAACTCAAGAG-ATAFAGAAGGGTAT--GTTAATCTTTGAACTAGGGTTTTT	2375
Db	1680	ATATCTTCAAACTCAAGAGCATATAGAAAGGTGTATGCTTAACTTTGAACTAGGGTTTTT	1739
Qy	2376	GATCCCTAACTCAATAGTAATCTTTTGTCTCCAATAGCCATGCTCTTTGCAATTTGCAG	2435
Db	1740	GATCCCTAACTCAATAGTAATCTTTTGTCTCCAATAGCCATGCTCTTTGCAATTTGCAG	1799
Qy	2436	ATCTAAGCTCTAATTGATGCCATAGTAAGAAAAATAAGATCTGTAGTTTTCCACTCGCTCAC	2495
Db	1800	ATCTAAGCTCTAATTGATGCCATAGTAAGAAAGATAGATCTGTAGTTTTCCACTCGCTCAC	1859
Qy	2496	TGAGTTCGAGTTTTAAATGAAGTGTCTGTTTTCTTTTTTCAATAT-AGTTGCAACTGGATT	2554
Db	1860	TGAGTTCGAGTTTTAAATGAAGTGTCTGTTTTCTTTTTTCAATATAGTTCGAACTGGATT	1919
Qy	2555	ATAATTA AAAAATATATATGGACGAGAAAAATAATTA AAAATAGATATAGATAACAATGTC	2614
Db	1920	ATAATTA AAAAATATATATGGACGAGAAAAATAATTA AAAATAGATATAGATAACAATGTC	1979
Qy	2615	AAATTGAGAAATTTTTTATAGAAGAATAATTA ACTTACAGTTGTTTTTTTTTTCAGCTGT	2674
Db	1980	AAATTGAGAAATTTTTTATAGAAGAATAATTA ACTTACAGTTGTTTTTTTTTTCAGCTGT	2039
Qy	2675	AAAAGAAATCTAATTTGTTCTCACGACTGTGCTTCATCTTTTGGAAAATCTAAGCAAAG	2734
Db	2040	AAAAGAAATCTAATTTGTTCTCACGACTGTGCTTCATCTTTTGGAAAATCTAAGCAAAG	2099
Qy	2735	AAAATGTTTAAACTCGGATCTTAAGATTATGAACCTCGTAATATAAAAACACTATATAGTAT	2794
Db	2100	AAAATGTTTAAACTCGGATCTTAAGATTATGAACCTCGTAATATAAAAACACTATATAGTAT	2159
Qy	2795	TAAATTTGAACCTAGTGTGTCTTTTGTCTACTTTTGACTTTTGAATAATAAACTGGAACA	2854
Db	2160	TAAATTTGAACCTAGTGTGTCTTTTCTCTA-TTTGACTTTAGAAATTA AAACCTGAAACA	2218
Qy	2855	AAGATGTCAAATCTGAGTAGGGAGTCTTTGACCTCTGGGGATCCATAAAAAGAACTAACT	2914
Db	2219	AAGATGTCAAATCTGAGTAGGGAGTCTTTGACCTCTGGGGATCCATAAAAAGAAATTA ACT	2278
Qy	2915	CCATCTTAAATCGGCTTCTTACCGATGGTCAAACTTAGCTTCCAAACAGCAACAGCTGTT	2974

2279	CCATCCTTAAAAATCGGCTTCTTACCGATTGGTCAAACTTAGCTCCAAACAAGCAAACAGCTGT	2333
2975	CTTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGCATTTGTCCTCTCTCGAAAAAATAAAG	3034
2339	CTTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGCATTTGTCCTCTCTCGAAAAAATAAAG	2398
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2399	ATTGGTAAATTGGCAAGATTATAATTAATTTATTAATGTGTGCATCTAAGAAGATTTT	2458
3094	CTGTACTTAATTGTAGCAAAAATTAAAGAAACCCGAGTTAGAACTCGAAGCTAAGAGCATYA	3153
2459	CTGTACTTAATTGTAGCAAAAATTAAAGAAACCCGAGTTAGAACTCGAAGCTAAGAGCATYA	2518
3154	GGGTCTATGAATTCATCTCTGTTTGTTTATTATTAAGGTTATCATAGAGATCGGTACTTGATT	3213
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3214	TGTTATAGGAAATCTTGGTTTAAATTCGCATAAAACCATCAATTAGATTTATTCCTAAAAATGTG	3273
2579	TGTTATAGGAAATCTTGGTTTAAATTCGCATAAAACCATCAATTAGATTTATTCCTAAAAATGTG	2638
3274	ATGATATTTTGGTGCANCTCCATATATTATTATATAATAAATGATAAATTGGTTGATGAT	3333
2639	ATGATATTTTGGTTACATCTCCATATATTATTATATAATAAATGATAAATTGGTTGATGAT	2698
3334	AAGCTTAAACCCCTAAATCTCTGGAATCATCAGTATGAGAGAATACTTTGAACGCTATGAGA	3393
2699	AAGCTTAAACCCCTAAATCTCTGGAATCATCAGTATGAGAGAATACTTTGAACGCTATGAGA	2758
3394	GGTACTCTTACGCCGAAAGACAGCTTATTGCACCTCAGTCCGACGCTCAATGTATTTCCAAT	3453
2759	GGTACTCTTACGCCGAAAGACAGCTTATTGCACCTCAGTCCGACGCTCAATGTATTTCCAAT	2818
3454	AAATATTCTCTCTTTTAAATCCCATATATATTATATCAATCTATTGTGTAGTATTGATGAA	3513
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3514	TTTTTATTGTATAAAACTTCTCGTACACAGACAACTGGTCCGATGCAGTATACAGGCTT	3573
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3634	CTATCTAGAAAATCGAATCGGGTTCATTTTAAAGTAAGTTAAAAATTCATTGATGCTATTG	3693
2999	CTATCTAGAAAATCGAATCGGGTTCATTTTAAAGTAAGTTAAAAATTCATTGATGCTATTG	3058
3694	AAATTCAGGCAATATCTTTGGGGAAGACTTGCAGCAAAATGAGCCCTTAAAGAGCTTCAGAA	3753
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3754	CTGGAGCAGCAGCTTGACACTGCTTTAAGCACATCCGACCTPAGAAAAAGTATTGCTCTCT	3813
3119	CTGGAGCAGCAGCTTGACACTGCTTTAAGCACATCCGCACTAGAAAAAGTATTGCTCTCT	3178
3814	GCTATTTGCTTGAACATATCTATAATAACTTAAACGTTTACAGTGTATTATATAATGTGAA	3873
3179	GCTATTTGCTTGAACATATCTATAATAACTTAAACGTTTACAGTGTATTATATAATGTGAA	3238
3874	CATTGAAATACATATGTGTATGTATCAATATATATATCAGTAAATCAATATCAATTTGATA	3933
3239	CATTGAAATACATATGTGTATGTATCAATATATATATCAGTAAATCAATATCAATTTGATA	3298
3934	TGCTCTATAGTTTGGTTTCGAAATGATGAGTTATGTTGTGATTTTAAAGACTCCATATTACT	3993
3299	TGCTCTATAGTTTGGTTTCGAAATGATGAGTTATGTTGTGATTTTAAAGACT-CATATTACT	3357
3994	TAAAGTAAATGGGTTGTTAAATGTTGATGTGTGTATGCAGAACCAACCTTATGTACAGTGC	4053
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QY	4054	CATCAATGAGCTCCAAAAAAGGTATGTAACCCCTATCAAATGTATGCTTATAGAGA	4113
Db	3418	CATCAATGAGCTCCAAAAAAGGTATGTAACCCCTATCAAATGTATGCTTATAGAGA	3477
QY	4114	AACGTATAGAAAGCTAAATTAAACAATCGTGCGGTTCGGAAATGA CAGGAGAGGCCATA	4173
Db	3478	AACGTATAGAAAGCTAAATTAAACAATCGTGCGGTTCGGAAATGA CAGGAGAGGCCATA	3537
QY	4174	CAGGAGCAAAACAGCATGCTTTCTAAACAGGTAAACACATGTATCATTTCTCTTTTCATCA	4233
Db	3538	CAGGAGCAAAACAGCATGCTTTCTAAACAGGTAAACACATGTATCATTTCTCTTTTCATCA	3597
QY	4234	ACATGTTGTCATTTGCATTAAGTACTTCCACTGTTCTGCTCCACACTTCOCAGCCAAG	4293
Db	3598	ACATGTTGTCATTTGCATTAAGTACTTCCACTGTTCTGCTCCACACTTCOCAGCCAAG	3657
QY	4294	CTATACCTACGATATCTTCATCTCCATTAACCTTCGGCACCATTAATAAATAAATAGAA	4353
Db	3658	CTATACCTACGATATCTTCATCTCCATTAACCTTCGGCACCATTAATAAATAAATAGAA	3717
QY	4354	AATCTTTGCAAAATTTGTTTCAAAATAGCATAGATGTTGTCATTAAGTTGATATTAATCACCA	4413
Db	3718	AATCTTTGCAAA- TTGTTTGAATAGATAGATGTTGTCATTAAGTTGATATTAATCACCA	3776
QY	4414	GCCTGTACGTAGATATGGTTTGTCGGTTTAGTTTTAAG- TGCTCTCGGATTTGAAAATA	4472
Db	3777	GCCTATACGTAGATATGGTTTGTCGGTTTAGTTTTAAGTTGCTCTCGGATTTGAAAATA	3836
QY	4473	TTTTTGAATCTTTTGAATGTTTGTCGCCATCATTTCTTACTAGTCTCATATCTATGTATAT	4532
Db	3837	TTTTTGAAT- - - - CTTTGAATGTTTGTCGCCATCATTC- TACTTAGTCTCATATCTATGTATAT	3891
QY	4533	GAAATATAGACACTACTCCTAATTAAT- AAAAAATGTTTATTAATAGTTCAATPGCAAGTGCAC	4591
Db	3892	GAAATATAGACACTACTCCTAATTAATAAAAAATGTTTATTAATAGTTCAATPGCAAGTGCAC	3951
QY	4592	TGTGAAAAATAACTATTTTGTAAACCATTGCATATATATAGTTTCTTCACTTTGAAAAATTGAT	4651
Db	3952	TGTGAAAAATAACTATTTTGTAAACCATTGCATATATATAGTTTCTTCACTTTGAAAAATTGAT	4011
QY	4652	GATCATATATGTTTGCATAATAAATTTTGTGGCAGATCAAGGAGAGGAGAAAAATTCCTTA	4711
Db	4012	GATCATATATGTTTGCATAATAAATTTTGTGGCAGATCAAGGAGAGGAGAAAAATTCCTTA	4071
QY	4712	GGGCTCAACAGGAGCAGTGGGATCAGCAGAAACCAAGGCCACAATATGCCCTCCCCTCTGC	4771
Db	4072	GGGCTCAACAGGAGCAGTGGGATCAGCAGAAACCAAGGCCACAATATGCCCTCCCCTCTGC	4131
QY	4772	CACCGCAGCAGCAACCAATCCAGCATCCTTACATGCTCTCTCATCAGCAGCATCTCCTTTTC	4831
Db	4132	CACCGCAGCAGCAACCAATCCAGCATCCTTACATGCTCTCTCATCAGCAGCATCTCCTTTTC	4191
QY	4832	TCAACATGGGTAAACAAAAATTACTAATCATGTTAAATTPAAAGCACATATGTTATGCA	4891
Db	4192	TCAACATGGGTAAACAAAAATTACTAATCATGTTAAATTPAAAGCACATATGTTATGCA	4951
QY	4892	AGCTAGTTACGTTAGGTGTTGCTTAATTTCAATGAGTTTATAGCTGTAGTCAATGCTTACAT	4951
Db	4252	AGCTAGTTACGTTAGGTGTTGCTTAATTTCAATGAGTTTATAGCTGTAGTCAATGCTTACAT	4311
QY	4952	GATG- CTAGATTTTGAACCTAGAAAACTTATTTTAAACATTAATTTTATTAACGTAGGT	5010
Db	4312	GATGTCATGATTTTGAACCTAGAAAACTTATTTTAAACATTAATTTTATTAACGTAGGT	4371
QY	5011	TAATGCAATGTCGCCAAACGAAACAACTTATTAGTGTGGAATAATGTACATGGAATGGT	5070
Db	4372	TAATGCAATGTCGCCAAACGAAACAACTTATTAGTGTGG- AAATGTACATGGAATGGT	4430
QY	5071	TGCGAAAAAGCCCTAAGTCGCAC- TTTTGTGTTGTTGGTCTATGTGTTTAAAGTACAAATTTTA	5129
Db	4431	TGCGAAAAAGCCCTAAGTCGCAC- TTTTGTGTTGTTGGTCTATGTGTTTAAAGTACAAATTTTA	4490

	Qy	5130	GTTTGTAGATAAATGAAATTATATATCTTTTGACATTTTCACAATGGACTGATATTGGAT	5189
	Db	4491	GTTTGTAGATAAATGAAATTATATCTTTTGACATTTTCACAATGGACTGATATTGGAT	4550
	Qy	5190	TTTTCCCTTTGTGTACCGTGAAAACATATGATTACATATGCACITTCATATATATCCTATGT	5249
	Db	4551	TTTTCCCTTTGTGTACCGTGAAAACATATGATTACATATGCACITTCATATATATCCTATGT	4610
	Qy	5250	ATGATTGTGAATGCAGTGGTCTGTATCAAGAAGATGCCAATGGCAATGAGGAGGAATG	5309
	Db	4611	ATGATTGTGAATGCAGTGGTCTGTATCAAGAAGATGCCAATGGCAATGAGGAGGAATG	4670
	Qy	5310	ATTCGAACTGACTCTTGAAACCGGTTTACAACTGCAACCTT	5350
	Db	4671	ATTCGAACTGACTCTTGAAACCGGTTTACAACTGCAACCTT	4711

  

RESULT 7		4712 bp	DNA	linear	PLN 15-MAY-2002
AF466773	Arabidopsis thaliana Chi-1 apetala 1 (AP1) gene, partial cds.				
DEFINITION	AF466773				
VERSION	AF466773.1	GI:20799343			
KEYWORDS					
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi				
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purganan,M.D.				
TITLE	Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral Developmental Pathway				
JOURNAL	Genetics 160 (4), 1641-1650 (2002)				
MEDLINE	21969421				
PUBMED	11973317				
REFERENCE	2 (bases 1 to 4712)				
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purganan,M.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-JAN-2002) Genetics, North Carolina State University, Campus Box 7614, Raleigh, NC 27695-7614, USA				
FEATURES	Location/Qualifiers				
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Query Match	82.9%	Score 4451;	DB 8;	Length 4712;
Best local similarity	98.8%	Pred.No. 0;		
Origin				

Matches 4664; Conservative 0; Mismatches 35; Indels 22; Gaps 17;

QY	643	AGGCTTATGCAATATATAGCCTTAAGCAAAATCCGAATCTG- TTTTTTTTTTTTTGTATTG	701
Db	1	AGGCTTATGCAATATATAGCCTTAAGCGAATCCGAATCTGTTTTTTTTTTTTTTTGTATTG	60
QY	702	GATATTGACTGAAATAGGGGTTTTTTCACACTTTGAAGATCTCAAAGAGAAAACTATT	761
Db	61	GATATTGACTGAAATAGGGGTTTTTTCACACTTTGAAGATCTCAAAGAGAAAACTATT	120
QY	762	ACAAACGGAAATTCATTGTAAAGAAGTGAATTAAGCAAAATTCAGACAAAGTTTTTATGTGG	821
Db	121	ACAACGGAAATTCATTGTAAAGAAGTGAATTAAGCAAAATTCAGACAAAGTTTTTATGTGG	180
QY	822	TTTATTTCAATATATGATGATGACATCAAAATGTTATATATATGTTGTTTTTATTTAACAA	881
Db	181	TTTATTTCAATATATGATGATGACATCAAAATGTTATATATATGTTGTTTTTATTTAACAA	240
QY	882	TATATGGATATAACGTCACAACTAAATATGTTTGCAATTCAGCAAAAAATATATGTTATG	941
Db	241	TATATGGATATAACGTCACAACTAAATATGTTTGCAATTCAGCAAAAAATATATGTTATG	300
QY	942	TTGATTAAACAATAGACATATTCAACTGATTTTTTGTCTGTGATCATCTACAACCTTA	1001
Db	301	TTGATTAAACAATAGACATATTCAACTGATTTTTTGTCTGTGATCATCTACAACCTTA	360
QY	1002	AGAACACACAATTTGAAAAAATCTTTTGACAAAATACTATTTTTGGGTTTGAATTTTGA	1061
Db	361	AGAACACACAATTTGAAAAAATCTTTTGACAAAATACTATTTTTGGGTTTGAATTTTGA	420
QY	1062	ATACTTTACAATTTCTTCTCGATCTTCTCTCTCTTTTCTTAAATCTCTGCGTACAAATCCG	1121
Db	421	ATACTTTACAATTTCTTCTCGATCTTCTCTCTCTTTTCTTAAATCTCTGCGTACAAATCCG	480
QY	1122	TCGACGCAATACATTACACAGTTGTCGAAATGGTTCTCAGCTCTACCAAAACATCTATTG	1181
Db	481	TCGACGCAATACATTACACAGTTGTCGAAATGGTTCTCAGCTCTACCAAAACATCTATTG	540
QY	1182	CCAAAAGAAAGTGCTATTTTGTACTTCACTGTTACAGCTGAGAACATTTAAATATAATAAGC	1241
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QY	1242	AAATTTGATAAAACAAAGGGTTCTACCTTTATTCCAAAGAAATAGTGTAAAAATAGGGTAA	1301
Db	601	AAATTTGATAAAACAAAGGGTTCTACCTTTATTCCAAAGAAATAGTGTAAAAATAGGGTAA	660
QY	1302	TAGAGAA- ATGTTTAAATAAAGGAAATTAANAATAGATATTTTGGTTGGTTTCAGATTTGT	1360
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QY	1361	TTCGTAGATCTACAGGAAATCTCCGCGTCAATGCAAGCGAAGGTGACATCTTGGGAA	1420
Db	721	TTCGTAGATCTACAGGAAATCTCCGCGTCAATGCAAGCGAAGGTGACATCTTGGGAA	780
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Db	781	GGACCAAGTGGTCGTTACAATGTTACTTTACCCATTTCTTTTTCACAGACGTCGATAATCAA	840
QY	1481	ATTGTTTATTTTTCATATTTTTTAAAGTCCGAGTTTTTATTAANAATCATGACCCGACATT	1540
Db	841	ATTGTTTATTTTTCATATTTTTTAAAGTCCGAGTTTTTATTAANAATCATGACCCGACATT	900
QY	1541	AGTACGAGATATACCAATGAGAAAGTGCACACGCAAAATCTTAAAGAAACCACTGTGTTTT	1600
Db	901	AGTACGAGATATACCAATGAGAAAGTGCACACGCAAAATCTTAAAGAAACCACTGTGTTTT	960
QY	1601	TGCAAAACAGAGAAAACAGCTTTTAGCTTTTCCCTTAAACCACTCTTACCCAAATCTCTCC	1660
Db	961	TGCAAGCAAGAGAAAACAGCTTTTAGCTTTTCCCTTAAACCACTCTTACCCAAATCTCTCC	1020
QY	1661	ATAAATAAGATCCCGAGACTCAAAACAAGTCTTTTTTATAAGGAAAGAGAAAAACT	1720
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DEFINITION AP466777

ACCESSION AP466777

VERSION AP466777.1 GI:20799351

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 4709)

AUTHORS Olsen, K.M., Womack, A., Garrett, A.R., Suddith, J.I. and Purugganan, M.D.

TITLE Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral Developmental Pathway

JOURNAL Genetics 160 (4), 1641-1650 (2002)

MEDLINE 21969421

PUBMED 11973317

REFERENCE 2 (bases 1 to 4709)

AUTHORS Olsen, K.M., Womack, A., Garrett, A.R., Suddith, J.I. and Purugganan, M.D.

TITLE Direct Submission

JOURNAL Submitted (09-JAN-2002) Genetics, North Carolina State University, Campus Box 7614, Raleigh, NC 27695-7614, USA

FEATURES

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				Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral	

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Fri Oct 1 13:40:13 2004

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 REFERENCE 1 (bases 1 to 4707)  
 AUTHORS Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and  
 Purugganan,M.D.  
 TITLE Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral  
 Developmental Pathway  
 JOURNAL Genetics 160 (4), 1641-1650 (2002)  
 MEDLINE 21969421  
 PUBMED 11973317  
 REFERENCE 2 (bases 1 to 4707)  
 AUTHORS Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and  
 Purugganan,M.D.  
 TITLE Direct Submission  
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VERSION	AF466785.1	GI:20799367			
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ORGANISM	Arabidopsis thaliana				
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REFERENCE	1 (bases 1 to 4706)				
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purganan,M.D.				
TITLE	Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral Developmental Pathway				
JOURNAL	Genetics 160 (4), 1641-1650 (2002)				
MEDLINE	21969421				
PUBMED	11973317				
REFERENCE	2 (bases 1 to 4706)				
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purganan,M.D.				
	Arabidopsis thaliana				
TITLE	Direct Submission				
JOURNAL	Submitted (09-JAN-2002) Genetics, North Carolina State University, Campus Box 7614, Raleigh, NC 27695-7614, USA				
FEATURES	Location/Qualifiers				
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	source				

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 Olsen, K.M., Womack, A., Garrett, A.R., Suddith, J.I. and  
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QY 3992 CTTAAAGTAATGGGTTGTTTAAATGTTGATGTTGTTATGTTGTTATGTTGTTATGTTGTTATG 4051
Db 3358 CTTAAAGTAATGGGTTGTTTAAATGTTGATGTTGTTATGTTGTTATGTTGTTATGTTGTTATG 3417
QY 4052 TCCATCAATGAGCTCCAAAAAAGGTATGTAACACCCCTATCAAAATGATGTTCTTATAGA 4111
Db 3418 TCCATCAATGAGCTCCAAAAAAGGTATGTAACACCCCTATCAAAATGATGTTCTTATAGA 3477
QY 4112 GAAACGTATAGAAAGCTTAATTAACAATCGTCCGTTTCGAAATGACAGGAGAGGCCA 4171
Db 3478 GAAACGTATAGAAAGCTTAATTAACAATCGTCCGTTTCGAAATGACAGGAGAGGCCA 3537
QY 4172 TACAGGAGCAAAACAGATGCTTTCTAAACAGGTAACACATGTCATCTTCTTTTCAAT 4231
Db 3538 TACAGGAGCAAAACAGGATGCTTTCTAAACAGGTAACACATGTCATCTTCTTTTCAAT 3597
QY 4232 CAACATGTTGTCATTTGCAATGTTTACCTTCCACTGTTCTGCTCCACACTTCCAGCCA 4291
Db 3598 CAACATGTTGTCATTTGCAATGTTTACCTTCCACTGTTCTGCTCCACACTTCCAGCCA 3657
QY 4292 AGCTATACCTAGATATCTTCATATCTCCACTTAACCTTCGGCACCATTAAATAAAATAG 4351
Db 3658 AG-----ACCTAGCATATCTTCATATCTCCACTTAACCTTCGGCACCATTGAATAAAATAG 3713
QY 4352 AAAATCTTGCATAATTTCTTGAATAGCATAGATGTTGCTATGTTGATGATGATGATGATGATG 4411
Db 3714 AAAATCTTGCATAATTTCTTGAATAGCATAGATGTTGCTATGTTGATGATGATGATGATGATG 3772
QY 4412 CAGCCTGATAGATATGTTGCTCGTTTGTAGTTTAAAGG-TGCTCTCGGATTGAAA 4470
Db 3773 CAGCCTGATAGATATGTTGCTCGTTTGTAGTTTAAAGGTTGCTCGGATTGAAA 3832
QY 4471 TATTTTGAATCTTTTGAATGTTTGTCCCATCTTCTTACTAGCTCATATCTATGTTAT 4530
Db 3833 TATTTTGAATCTTTTGAATGTTTGTCCCGTCTATTC-TACTTAGCTCATATCTATGTTAT 3887
QY 4531 ATGAATATAGACACTACTCTTAATTAT-AAAATGTTATATAGTTTCAATGATGATGATGATG 4589
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QY 4710 TAGGGCTCAACAGGAGCAGTGGGATCAGCAGAACCAAGGCCACAAATATGCTTCCCTCTCT 4769
Db 4068 TAGGGCTCAACAGGAGCAGTGGGATCAGCAGAACCAAGGCCACAAATATGCTTCCCTCTCT 4127
QY 4770 GCCACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 4829
Db 4128 GCCACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 4187
QY 4830 TCTCAACATGGGGTAAACAAAAATTTACTAATCAGTCTTAAATTTAAAGCAGATATGTTATG 4889
Db 4188 TCTCAACATGGGGTAAACAAAAATTTACTAATCAGTCTTAAATTTAAAGCAGATATGTTATG 4247
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